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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:38:20 ; Search time 102.423 Seconds
(without alignments)
1488.535 Million cell updates/sec

Title: US-10-070-532-2
Perfect score: 2219
Sequence: 1 MEPSATPGAQMGVPPGSREP.....CSVSKISEHVVLTSVTTVLP 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2219	100.0	425	4	AAU00438	Aau00438 Human neu
2	2218	100.0	425	4	AAB67489	Aab67489 Amino aci
3	2215	99.8	425	4	AAU11188	Aau11188 Human G p
4	2215	99.8	425	8	ADL22443	Adl22443 Human ore
5	2214	99.8	425	2	AAW80456	Aaw80456 G-protein
6	2214	99.8	425	4	AAU11186	Aau11186 Human G p
7	2214	99.8	425	4	AAB67079	Aab67079 Human HFG
8	2214	99.8	425	5	AAG78345	Aag78345 Human HFG
9	2214	99.8	425	6	ABP81941	Abp81941 Human ore

10	2214	99.8	425	7	ABG75058	Abg75058	Human ore
11	2214	99.8	425	7	ADK52564	Adk52564	Hematolog
12	2214	99.8	425	8	ADL22428	Adl22428	Human ore
13	2214	99.8	425	8	ADO29106	Ado29106	Human nov
14	2209	99.5	425	4	ABB56378	Abb56378	Non-endog
15	2183	98.4	425	4	AAE04740	Aae04740	Cynomolgo
16	2097	94.5	402	2	AAW06124	Aaw06124	Neuropept
17	2093.5	94.3	401	5	AAG78346	Aag78346	Human HFG
18	2087	94.1	427	4	AAB47300	Aab47300	Dog orexi
19	2019.5	91.0	416	8	ADO29107	Ado29107	Mouse nov
20	1908	86.0	364	4	AAU00442	Aau00442	Human neu
21	1902.5	85.7	389	2	AAW80805	Aaw80805	Amino aci
22	1902.5	85.7	389	4	AAU11187	Aau11187	Human G p
23	1902.5	85.7	389	5	ABB08208	Abb08208	G-protein
24	1898	85.5	377	2	AAW06126	Aaw06126	Neuropept
25	1897	85.5	369	2	AAW06125	Aaw06125	Neuropept
26	1897	85.5	372	4	AAU00440	Aau00440	Human neu
27	1869	84.2	369	4	AAU00439	Aau00439	Human neu
28	1478.5	66.6	443	8	ADO29110	Ado29110	Mouse nov
29	1474.5	66.4	460	4	AAB61970	Aab61970	Rat HCRT
30	1474.5	66.4	460	6	ABG73515	Abg73515	Rat OX2R
31	1469	66.2	444	4	AAB61968	Aab61968	Canine wi
32	1463	65.9	444	4	AAB84416	Aab84416	Amino aci
33	1460	65.8	444	4	AAB98007	Aab98007	Human hyp
34	1460	65.8	444	4	AAB61969	Aab61969	Human HCR
35	1460	65.8	444	6	ABG73514	Abg73514	Human OX2
36	1460	65.8	444	6	ABP81942	Abp81942	Human ore
37	1460	65.8	444	7	ABG75059	Abg75059	Human ore
38	1460	65.8	444	8	ADO29109	Ado29109	Human nov
39	1459	65.8	444	2	AAU03649	Aay03649	Human 7-t
40	1455	65.6	444	4	ABB56379	Abb56379	Non-endog
41	1311	59.1	263	2	AAR91233	Aar91233	Rabbit G-
42	1311	59.1	263	2	AAW11236	Aaw11236	G-protein
43	1164.5	52.5	330	4	AAB61971	Aab61971	Canine na
44	997	44.9	327	4	AAB61972	Aab61972	Canine na
45	525	23.7	430	8	ADJ87508	Adj87508	Murine re

ALIGNMENTS

RESULT 1

AAU00438

ID AAU00438 standard; protein; 425 AA.

XX

AC AAU00438;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;

KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;

KW cardiovascular disorder; autoimmune disorder; infectious disorder;

KW eating behaviour disorder; narcolepsy; neurological disease;

KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;

KW protein co-ordinate data.

XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 47. .72
 FT /label= TM1
 FT /note= "Transmembrane region 1"
 FT Region 83. .106
 FT /label= TM2
 FT /note= "Transmembrane region 2"
 FT Region 112. .142
 FT /label= TM3
 FT /note= "Transmembrane region 3"
 FT Region 163. .189
 FT /label= TM4
 FT /note= "Transmembrane region 4"
 FT Region 214. .239
 FT /label= TM5
 FT /note= "Transmembrane region 5"
 FT Region 299. .327
 FT /label= TM6
 FT /note= "Transmembrane region 6"
 FT Region 335. .363
 FT /label= TM7
 FT /note= "Transmembrane region 7"
 XX
 PN WO200117532-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024518.
 XX
 PR 10-SEP-1999; 99US-00393696.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA;
 XX
 DR WPI; 2001-183276/18.
 DR N-PSDB; AAS00491.
 XX
 PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
 PT useful for preventing, treating or ameliorating obesity, narcolepsy,
 PT neurological disease and addiction to narcotics, nicotine and alcohol.
 XX
 PS Claim 3; Fig 4; 385pp; English.
 XX
 CC The present sequence represents a novel human neuropeptide receptor which
 CC shows sequence homology to the neuropeptide Y receptor. Two splice
 CC variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible
 CC mutant (AAU00442) are also described. Polypeptides and polynucleotides of
 CC the neuropeptide receptor are useful for diagnosing, preventing, or
 CC treating a pathological condition in a subject related to the central
 CC nervous and peripheral nervous systems (CNS and PNS). The polypeptides
 CC and polynucleotides may be used to treat hyperproliferative,
 CC cardiovascular, autoimmune, nervous system or infectious disorders e.g.
 CC cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV

CC infection and diabetes mellitus. In particular they are useful for
CC preventing, treating or ameliorating a medical condition in a mammal such
CC as obesity/eating behaviour disorders, narcolepsy, neurological disease,
CC addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,
CC migraine headaches and anxiety disorders. The polynucleotides encoding
CC the neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases

XX

SQ Sequence 425 AA;

Query Match 100.0%; Score 2219; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.1e-221;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFIAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFIAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKI SEHVVLTSV 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKI SEHVVLTSV 420

Qy    421 TTVLP 425
        |||||
Db    421 TTVLP 425
```

RESULT 2

AAB67489

ID AAB67489 standard; protein; 425 AA.

XX

AC AAB67489;

XX

DT 29-MAY-2001 (first entry)

XX

DE Amino acid sequence of a human hypocretin (orexin) receptor 1.

XX

KW Human; hypocretin receptor 1; orexin receptor 1; HCRT1; chromosome 1;
KW 1p33; central nervous system modulator.
XX
OS Homo sapiens.
XX
PN WO200114555-A1.
XX
PD 01-MAR-2001.
XX
PF 22-AUG-2000; 2000WO-US022986.
XX
PR 23-AUG-1999; 99US-00379083.
PR 07-JAN-2000; 2000US-00479128.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Olafsdottir BR, Gulcher J;
XX
DR WPI; 2001-211306/21.
DR N-PSDB; AAF55159.
XX
PT Novel isolated nucleic acid molecule encoding hypocretin (orexin)
PT receptor 1 useful for treating and diagnosing narcolepsy.
XX
PS Disclosure; Fig 1A; 44pp; English.
XX
CC The present sequence represents a human hypocretin (orexin) receptor 1
CC (HCRT1) polypeptide. The HCRT1 gene is present on chromosome 1,
CC location 1p33. It is likely that a mutation in the HCRT1 gene is
CC associated with narcolepsy. HCRT1 is a central nervous system modulator.
CC The HCRT1 polypeptide and polynucleotide are useful for diagnosing or
CC treating narcolepsy in an individual. The HCRT1 polynucleotide is a
CC source of probes and primers, and is also used to produce the protein
CC recombinantly
XX
SQ Sequence 425 AA;

Query Match 100.0%; Score 2218; DB 4; Length 425;
Best Local Similarity 99.8%; Pred. No. 1.4e-221;
Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA	180
Qy	181	AVMECSSVLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240

Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDL EQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDL EQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVLLLVFALCYLPISVLNV LKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVLLLVFALCYLPISVLNV LKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQFKAAFS CCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 |||: |||
 Db 361 LSGKFREQFKAAFS CCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy 421 TTVLP 425
 ||||
 Db 421 TTVLP 425

RESULT 3

AAU11188

ID AAU11188 standard; protein; 425 AA.

XX

AC AAU11188;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X variant.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;
 KW fungal infection; protozoan infection; viral infection;
 KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
 KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
 KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
 KW obesity; Kallman's syndrome; hypothalamic disorder;
 KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
 KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

DR N-PSDB; AAS17464.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.

XX

PS Claim 23; Fig 6; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.
CC infections such as bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
CC Huntington's disease and many other diseases and disorders given in the
CC specification. The present sequence is the human HFGAN72X variant,
CC encoded by an alternative allele of HFGAN72

XX

SQ Sequence 425 AA;

Query Match 99.8%; Score 2215; DB 4; Length 425;

Best Local Similarity 99.8%; Pred. No. 2.8e-221;

Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPSVPDPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSRPSVPDPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSSALVRNWKRPDQGLDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
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Qy 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 Qy 421 TTVLP 425
 |||||
 Db 421 TTVLP 425

RESULT 4

ADL22443

ID ADL22443 standard; protein; 425 AA.

XX

AC ADL22443;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human orexin 1 receptor variant protein.

XX

KW polydipsia; single nucleotide polymorphism; SNP; orexin 1 receptor gene;

KW schizophrenia; human; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 408

FT /note= "The wild-type residue of Ile is substituted with

FT Val at this position following a single nucleotide

FT polymorphism in the encoding gene"

XX

PN JP2004041055-A.

XX

PD 12-FEB-2004.

XX

PF 10-JUL-2002; 2002JP-00201575.

XX

PR 10-JUL-2002; 2002JP-00201575.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

DR WPI; 2004-208085/20.

DR N-PSDB; ADL22427.

XX

PT Estimating whether subject has factor of polydipsia, comprises

PT determining single nucleotide polymorphism in orexin 1 receptor gene

PT and/or at least one polymorphism in linkage disequilibrium.

XX

PS Claim 11; Page; 31pp; Japanese.

XX

CC The invention relates to a novel method for estimating whether a subject

CC has a factor of polydipsia. The method comprises determining a single

CC nucleotide polymorphism (SNP) at position 1222 of a fully defined orexin

CC 1 receptor gene sequence of 1411 nucleotides, as given in the

CC specification, and/or at least one polymorphism in the linkage

CC disequilibrium from a biological sample obtained from a subject. A

CC polynucleotide of at least 10 contiguous bases comprising the SNP at

CC position 1222 is useful for estimating whether a subject comprises a
CC factor of polydipsia. A polypeptide having a polymorphic variation in the
CC human orexin 1 receptor or its fragment, or a transformed cell which
CC expresses the polypeptide is useful for the screening of a compound that
CC controls the function of the human orexin 1 receptor. The method allows
CC detection of polydipsia, which is a serious symptom of schizophrenia and
CC therefore useful in the selection of a treatment for preventing the
CC symptom. This sequence represents the variant protein following the SNP
CC at position 1222 of the 1411 nt human orexin 1 receptor gene of the
CC invention. Note: This sequence is not shown in the specification. It has
CC been created from the protein of SEQ ID No 2 and information provided in
CC claim 11 of the specification.

XX

SQ Sequence 425 AA;

Query Match 99.8%; Score 2215; DB 8; Length 425;
Best Local Similarity 99.8%; Pred. No. 2.8e-221;
Matches 424; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLTPKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLTPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTsALVRNWKRPsdQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTsALVRNWKRPsdQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRvFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRvFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAafSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
      |||
Db    361 LSGKFREQFKAafSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420

Qy    421 TTVLP 425
      ||||
Db    421 TTVLP 425
```

RESULT 5

AAW80456

ID AAW80456 standard; protein; 425 AA.

XX

AC AAW80456;

```

XX DT 26-JAN-1999 (first entry)
XX
DE G-protein coupled receptor (HFGAN72X) polypeptide.
XX
KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;
KW bulimia; asthma; Parkinson's disease; acute heart failure;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW benign prostatic hypertrophy; neurological disorder.
XX
OS Homo sapiens.
XX
PN EP875566-A2.
XX
PD 04-NOV-1998.
XX
PF 27-OCT-1997; 97EP-00308563.
XX
PR 30-APR-1997; 97US-00846704.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 1998-559432/48.
DR N-PSDB; AAV63468.
XX
PT New human G-protein coupled receptor HFGAN72X polypeptide and
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT infection, cancer and Parkinson's disease.
XX
PS Claim 1; Page 7-8; 24pp; English.
XX
CC The present sequence represents a G-protein coupled receptor (HFGAN72X)
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC diagnosing diseases related to over or under expression of HFGAN72X
CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC probes, or determining HFGAN72X protein or mRNA expression levels.
CC HFGAN72X polypeptides are also useful for screening for compounds which
CC affect activity of the protein. Diseases that can be treated with
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders
XX
SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 2; Length 425;
Best Local Similarity 99.5%; Pred. No. 3.6e-221;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
Db 1 MEPSATPGAQMGPVPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

```

Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFGHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSGKFREQKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV	420
Db	361	LSGKFREQKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV	420
Qy	421	TTVLP	425
Db	421	TTVLP	425

RESULT 6

AAU11186

ID AAU11186 standard; protein; 425 AA.

XX

AC AAU11186;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;
 KW fungal infection; protozoan infection; viral infection;
 KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
 KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
 KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
 KW obesity; Kallman's syndrome; hypothalamic disorder;
 KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
 KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.

XX

PS Claim 8; Fig 2; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.
CC infections such as bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
CC Huntington's disease and many other diseases and disorders given in the
CC specification. The present sequence is the human HFGAN72X receptor being
CC the product of a splice variant of HFGAN72

XX

SQ Sequence 425 AA;

Query Match . 99.8%; Score 2214; DB 4; Length 425;

Best Local Similarity 99.5%; Pred. No. 3.6e-221;

Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLKQYEWVLI AAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLKQYEWVLI AAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSI LGIWA VSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
```

Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRARAFLEVKQMRARRKTAKML 300
 |||

Db 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVEGMRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||

Db 301 MVVLLVFALCYLPISVLNVLKRVEGMRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 |||

Db 361 LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy 421 TTVLP 425
 |||

Db 421 TTVLP 425

RESULT 7

AAB67079

ID AAB67079 standard; protein; 425 AA.

XX

AC AAB67079;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor SEQ ID NO: 13.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;

KW truncation mutant; ligand; neurodegenerative disorder; pain;

KW eating disorder; behaviour disorder; mood disorder.

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;

XX

DR WPI; 2001-071483/08.

XX

PT Polynucleotides encoding Lig 72A polypeptides or their variants, which

PT are useful in the treatment of a disease or disorder associated with

PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,

PT neuropathic pain and back pain.

XX

PS Claim 8; Fig 7; 10lpp; English.

XX

CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions

XX

SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 4; Length 425;
Best Local Similarity 99.5%; Pred. No. 3.6e-221;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSIWAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
        ||||||||||||||||||||||||||||||||||||||||||||:||||||
Db    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy    421 TTVLP 425
        ||||
Db    421 TTVLP 425
```

RESULT 8

AAG78345

ID AAG78345 standard; protein; 425 AA.

XX

AC AAG78345;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;

KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor.

XX

OS Homo sapiens.

XX

PN EP1154019-A2.

XX

PD 14-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203008.

XX

PR 30-APR-1997; 97US-00846704.

PR 27-OCT-1997; 97EP-00308563.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-012659/02.

DR N-PSDB; AAI64172.

XX

PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.

XX

PS Claim 11; Page 7-8; 24pp; English.

XX

CC The present sequence is that of a human HFGAN72X polypeptide encoded by a
CC cDNA shown in AAI64172. The specification describes a newly isolated
CC polynucleotide encoding a HFGAN72X G coupled receptor polypeptide. The
CC protein of the invention has antibacterial, fungicide, virucide,
CC protozoacide, anti-HIV, cardiant, analgesic, cytostatic, nootropic,
CC antiparkinsonian, antiulcer, antiasthmatic, tranquiliser, neuroleptic,
CC antidepressant, anticonvulsant and osteopathic activities. HFGAN72X
CC polynucleotides (PNs) are used to express HFGAN72X in vivo, to treat
CC diseases requiring increased activity or expression of HFGAN72X; for
CC recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC PNs are used to identify (ant)agonists of HFGAN72X, useful
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC polypeptides that compete with ligands for binding to HFGAN72X proteins
CC are also useful therapeutically and diagnostically. HFGAN72X-related
CC diseases include infections (bacterial, viral, fungal or protozoal,
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC manic depression; delirium; dementia; severe mental retardation and

CC dyskinesias
XX
SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 5; Length 425;
Best Local Similarity 99.5%; Pred. No. 3.6e-221;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSI LGIWA VSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKI SEHVVLTSV 420
          |||
Db    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKI SEHVVLTSV 420

Qy    421 TTVLP 425
          |||
Db    421 TTVLP 425
```

RESULT 9

ABP81941

ID ABP81941 standard; protein; 425 AA.

XX

AC ABP81941;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 protein SEQ ID NO:368.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42789.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 6; Length 425;
 Best Local Similarity 99.5%; Pred. No. 3.6e-221;
 Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1 MEPSATPGAQMGVPPGSRPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSRPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLIGIWA VSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLIGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
        ||||||||||||||||||||||||||||||||||||||||||||:||||||
Db    361 LSGKFREQFKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420

Qy    421 TTVLP 425
        |||||
Db    421 TTVLP 425
  
```

RESULT 10

ABG75058

ID ABG75058 standard; protein; 425 AA.

XX

AC ABG75058;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human orexin receptor 1 protein.

XX

KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;

KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;

KW cardiatic; osteopathic; antilipemic.

XX

OS Homo sapiens.

XX

PN WO2003075945-A2.

XX

PD 18-SEP-2003.

XX
PF 14-MAR-2003; 2003WO-EP002714.
XX
PR 14-MAR-2002; 2002EP-00005882.
PR 15-MAR-2002; 2002EP-00006012.
PR 20-MAR-2002; 2002EP-00006271.
PR 25-MAR-2002; 2002EP-00006810.
XX
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;
XX
DR WPI; 2003-748334/70.
DR N-PSDB; ACH00818.
XX
PT New pharmaceutical composition comprising a nucleic acid molecule
PT encoding proteins regulating the energy homeostasis and metabolism of
PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
PT obesity.
XX
PS Claim 3; Fig 7G; 140pp; English.
XX
CC The present invention relates to pharmaceutical compositions comprising
CC the coding sequences shown in ACH00815-ACH00827, or their encoded
CC proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins
CC involved in the metabolism of triglycerides and in energy homeostasis,
CC and their coding sequences. The composition is useful for the manufacture
CC of an agent for detecting, verifying, treating, alleviating or preventing
CC disorders, including metabolic diseases such as obesity and other body-
CC weight regulation disorders as well as related disorders such as
CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
CC hypertension, coronary heart disease, hypercholesterolaemia,
CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,
CC organs or subjects. The coding sequences can be used in the production of
CC transgenic animals which under- or over-produce the gene of interest. The
CC present sequence is a protein of the invention
XX
SQ Sequence 425 AA;

Db 181 AVMECSSVLPELANRTRLFVSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLEVKQMRARRKTAKML 300
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 Db 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420
 Qy 421 TTVLP 425
 Db 421 TTVLP 425

RESULT 11

ADK52564

ID ADK52564 standard; protein; 425 AA.

XX

AC ADK52564;

XX

DT 06-MAY-2004 (first entry)

XX

DE Hematological disorder associated Gene ID 14393 encoded protein.

XX

KW cytostatic; antianemic; antisickling; virucide; hemostatic; nephrotropic;

KW cytostatic; thrombolytic; antiparasitic; gene therapy;

KW hematologic disorder; cancer; Sickle Cell Anemia;

KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;

KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;

KW transfusion reaction; Erythroblastosis; mechanical trauma;

KW micro-angiopathic hemolytic anemia; parasite infection.

XX

OS Homo sapiens.

XX

PN WO2003065871-A2.

XX

PD 14-AUG-2003.

XX

PF 28-JAN-2003; 2003WO-US002484.

XX

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

PR 26-APR-2002; 2002US-0375626P.

PR 06-JUN-2002; 2002US-0386494P.

PR 24-JUN-2002; 2002US-0390965P.

PR 28-JUN-2002; 2002US-0392480P.

PR 03-JUL-2002; 2002US-0394128P.

PR 31-JUL-2002; 2002US-0399783P.

PR 13-AUG-2002; 2002US-0403221P.

PR 30-AUG-2002; 2002US-0407045P.

PR 25-NOV-2002; 2002US-0429048P.

XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Carroll JM, Healy A, Weich NS, Kelly LM;
XX
DR WPI; 2003-731464/69.
DR N-PSDB; ADK52563.
XX
PT Identifying a compound capable of treating a hematologic disorder (e.g.
PT anemia or leukemia) comprises assaying the ability of the compound to
PT modulate the expression or activity of e.g. 131,148, 199 or 12303
PT polypeptide or nucleic acid.
XX
PS Disclosure; SEQ ID NO 22; 232pp; English.
XX
CC The invention relates to a method of identifying a compound capable of
CC treating a hematologic disorder comprises assaying the ability of the
CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
CC acid expression or polypeptide activity, thus, identifying a compound
CC capable of treating a hematologic disorder. The methods are useful in
CC diagnosing, preventing and treating hematological disorders, such as
CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
CC Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders
CC associated with an increased risk of Thrombosis, Herpes, Thalassemia,
CC antibody-mediated disorders such as transfusion reactions and
CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
CC angiopathic hemolytic anemias, infections by parasites or chemical
CC injuries. The methods may also be used for identifying compounds that
CC modulate hematological disorders. This sequence corresponds to the
CC protein encoded by one of the genes modulated by the compounds.
XX
SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 7; Length 425;
Best Local Similarity 99.5%; Pred. No. 3.6e-221;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||
```

Db 241 KIWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MIVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTTFSHWLVYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MIVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 ||||||||||||||||||||||||||||||||||||||||||||:|||||||
 Db 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420
 Qy 421 TTVLP 425
 |||||
 Db 421 TTVLP 425

RESULT 12

ADL22428

ID ADL22428 standard; protein; 425 AA.

XX

AC ADL22428;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human orexin 1 receptor protein.

XX

KW polydipsia; single nucleotide polymorphism; SNP; orexin 1 receptor gene;
 KW schizophrenia; human.

XX

OS Homo sapiens.

XX

PN JP2004041055-A.

XX

PD 12-FEB-2004.

XX

PF 10-JUL-2002; 2002JP-00201575.

XX

PR 10-JUL-2002; 2002JP-00201575.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

DR WPI; 2004-208085/20.

DR N-PSDB; ADL22427.

XX

PT Estimating whether subject has factor of polydipsia, comprises

PT determining single nucleotide polymorphism in orexin 1 receptor gene

PT and/or at least one polymorphism in linkage disequilibrium.

XX

PS Claim 3; SEQ ID NO 2; 31pp; Japanese.

XX

CC The invention relates to a novel method for estimating whether a subject
 CC has a factor of polydipsia. The method comprises determining a single
 CC nucleotide polymorphism (SNP) at position 1222 of a fully defined orexin
 CC 1 receptor gene sequence of 1411 nucleotides, as given in the
 CC specification, and/or at least one polymorphism in the linkage
 CC disequilibrium from a biological sample obtained from a subject. A
 CC polynucleotide of at least 10 contiguous bases comprising the SNP at
 CC position 1222 is useful for estimating whether a subject comprises a

CC factor of polydipsia. A polypeptide having a polymorphic variation in the
CC human orexin 1 receptor or its fragment, or a transformed cell which
CC expresses the polypeptide is useful for the screening of a compound that
CC controls the function of the human orexin 1 receptor. The method allows
CC detection of polydipsia, which is a serious symptom of schizophrenia and
CC therefore useful in the selection of a treatment for preventing the
CC symptom. This sequence represents the protein of the 1411 nt human orexin
CC 1 receptor gene of the invention.

XX

SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 8; Length 425;
Best Local Similarity 99.5%; Pred. No. 3.6e-221;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSAVLTLISFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSAVLTLISFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
Db    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
          |||
Db    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy    421 TTVLP 425
          |||
Db    421 TTVLP 425
```

RESULT 13

ADO29106

ID ADO29106 standard; protein; 425 AA.

XX

AC ADO29106;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human novel GPCR HCRT1, SEQ ID NO:205.

XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO2004040000-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-US028226.
 XX
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 PA (PRIM-) PRIMAL INC.
 XX
 PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
 XX
 DR WPI; 2004-390329/36.
 DR N-PSDB; ADO29780.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 PS Claim 1; SEQ ID NO 205; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of

CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 425 AA;

Query Match 99.8%; Score 2214; DB 8; Length 425;
Best Local Similarity 99.5%; Pred. No. 3.6e-221;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPFPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSREPSVPFPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTTALVRNWKRPDQIGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTTALVRNWKRPDQIGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAASFCCPLGPGCSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
      |||
Db    361 LSGKFREQFKAASFCCPLGPGCSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy    421 TTVLP 425
      ||||
Db    421 TTVLP 425
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ABB56378

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XX

OS Synthetic.

XX

XX

XX

XX

XX

XX

XX

DR N-PSDB; ABI98014.

XX

XX

XX

XX

Matches 422; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA 60

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 Qy 121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVQA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVQA 180
 Qy 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLWGRQIPGTTLSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 KLWGRQIPGTTLSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTKKML 300
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSGKFREQFKAASFCCPLGPGCSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 ||||||||||||||||||||||||||||||||||||||||||||:||||||
 Db 361 LSGKFREQFKAASFCCPLGPGCSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420
 Qy 421 TTVLP 425
 |||||
 Db 421 TTVLP 425

RESULT 15

AAE04740

ID AAE04740 standard; protein; 425 AA.

XX

AC AAE04740;

XX

DT 10-SEP-2001 (first entry)

XX

DE Cynomolgous Monkey Orexin 1 Receptor.

XX

KW Cynomolgous monkey; Orexin 1 Receptor; 7 Transmembrane Receptor family;

KW 7TM; gene therapy; vaccine; microbial infection; HIV-1; HIV-2; pain;

KW cancer; diabetes; obesity; anorexia; bulimia; urinary retention;

KW Parkinson's disease; acute heart failure; hypotension; hypertension;

KW osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;

KW asthma; allergy; benign prostatic hypertrophy; migraine; vomiting;

KW psychotic disorder; neurological disorder; anxiety; schizophrenia;

KW manic depression; depression; delirium; dementia; mental retardation;

KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome.

XX

OS Macaca fascicularis.

XX

PN W0200140259-A2.

XX

PD 07-JUN-2001.

XX

PF 04-DEC-2000; 2000WO-US032849.

XX

PR 02-DEC-1999; 99US-0168553P.

PR 28-NOV-2000; 2000US-00723781.

XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Ellis CE;
XX
DR WPI; 2001-408276/43.
DR N-PSDB; AAD09335.
XX
PT Novel Cynomolgous Monkey Orexin 1 Receptor polypeptides, for treating
PT infections, pain, cancer, diabetes, obesity, asthma, schizophrenia,
PT hypertension, urinary retention, Parkinson's disease and stroke.
XX
PS Claim 2; Page 28; 33pp; English.
XX
CC The present sequence is Cynomolgous Monkey Orexin 1 Receptor which is
CC structurally related to members of 7 Transmembrane Receptor (7TM) family.
CC The Orexin 1 Receptor polypeptide and polynucleotide are useful for
CC treating bacterial, fungal, protozoan and viral infections, particularly
CC infections caused by HIV-1 or HIV-2, pain, cancer, diabetes, obesity,
CC anorexia, bulimia, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, stroke, ulcers, asthma, allergies, benign
CC prostatic hypertrophy, migraine, vomiting, psychotic and neurological
CC disorders including anxiety, schizophrenia, manic depression, depression,
CC delirium, dementia and severe mental retardation, and dyskinesias, such
CC as Huntington's disease or Gilles de la Tourette's syndrome. The
CC polypeptide is also useful for structure-based design of its agonist,
CC antagonist or inhibitor. The polynucleotide is useful for chromosome
CC localisation studies and in gene therapy. The Orexin 1 Receptor
CC polypeptide and polynucleotide are also useful as vaccines
XX
SQ Sequence 425 AA;

Query Match 98.4%; Score 2183; DB 4; Length 425;
Best Local Similarity 98.1%; Pred. No. 6.1e-218;
Matches 417; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
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Db 1 MEPSATPGAQMRVPTGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFLVA 60
Qy 61 LVGNTLVCLAVWRNHMRVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120
|||||||||||||||||||||||||||||||||||||
Db 61 LVGNTLVCLAVWRNHMRVTNYFIVNLSLADVLVTAICLPVSLLDITESWLFEGHALCK 120
Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
|||||||||||||||||||||||||||||||||||||:||||
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAVMVPQA 180
Qy 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||||||||||||||||||||||||||||||||||||
Db 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
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Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVLIVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
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 Db 301 MVLIVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

 Qy 361 LSGKFREQFKAASFCCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
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 Db 361 LSGKFREQFKAASFCCCLPGPGPCGSLKAPSPRSSASHKSLSLQSRCSVSKLSEHVVLTSV 420

 Qy 421 TTVLP 425
 |||||
 Db 421 TTVLP 425

Search completed: October 14, 2004, 10:50:36
 Job time : 105.423 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:43:25 ; Search time 25.8791 Seconds
(without alignments)
1089.110 Million cell updates/sec

Title: US-10-070-532-2
Perfect score: 2219
Sequence: 1 MEPSATPGAQMGMVPPGSREP.....CSVSKISEHVLTSTVTVLP 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					Description
No.	Score	Match	Length	DB	ID		
1	2218	100.0	425	3	US-09-479-128-2		Sequence 2, Appli
2	2214	99.8	425	3	US-08-846-704-2		Sequence 2, Appli
3	2214	99.8	425	4	US-09-211-823C-22		Sequence 22, Appl
4	2108	95.0	402	3	US-08-846-704-4		Sequence 4, Appli
5	2104	94.8	402	4	US-08-462-509B-2		Sequence 2, Appli
6	2104	94.8	402	5	PCT-US95-05616-2		Sequence 2, Appli
7	1902.5	85.7	389	2	US-08-846-705-2		Sequence 2, Appli
8	1902.5	85.7	389	4	US-09-211-823C-23		Sequence 23, Appl
9	1901	85.7	377	5	PCT-US95-05616-6		Sequence 6, Appli
10	1897	85.5	369	4	US-08-462-509B-4		Sequence 4, Appli
11	1897	85.5	369	5	PCT-US95-05616-4		Sequence 4, Appli

12	1894	85.4	372	4	US-08-462-509B-6	Sequence 6, Appli
13	1460	65.8	444	4	US-09-426-290-2	Sequence 2, Appli
14	1459	65.8	444	3	US-09-119-788-2	Sequence 2, Appli
15	1311	59.1	263	3	US-08-513-974B-54	Sequence 54, Appl
16	1311	59.1	263	3	US-08-513-974B-376	Sequence 376, App
17	1311	59.1	263	4	US-09-461-436B-54	Sequence 54, Appl
18	522.5	23.5	430	3	US-09-255-368-8	Sequence 8, Appli
19	522.5	23.5	430	4	US-09-405-558-8	Sequence 8, Appli
20	507.5	22.9	432	3	US-09-255-368-2	Sequence 2, Appli
21	507.5	22.9	432	4	US-09-405-558-2	Sequence 2, Appli
22	499.5	22.5	420	3	US-09-255-368-6	Sequence 6, Appli
23	499.5	22.5	420	4	US-09-405-558-6	Sequence 6, Appli
24	499	22.5	417	4	US-09-405-558-44	Sequence 44, Appl
25	436	19.6	370	3	US-09-172-353-2	Sequence 2, Appli
26	436	19.6	370	3	US-09-172-353-3	Sequence 3, Appli
27	436	19.6	370	4	US-09-799-955-2	Sequence 2, Appli
28	436	19.6	370	4	US-09-799-955-3	Sequence 3, Appli
29	435.5	19.6	381	2	US-08-687-355A-4	Sequence 4, Appli
30	435.5	19.6	381	4	US-09-407-367-4	Sequence 4, Appli
31	434	19.6	370	3	US-08-513-974B-26	Sequence 26, Appl
32	434	19.6	370	3	US-08-513-974B-323	Sequence 323, App
33	434	19.6	370	3	US-09-172-353-5	Sequence 5, Appli
34	434	19.6	370	3	US-08-776-971-21	Sequence 21, Appl
35	434	19.6	370	3	US-08-776-971-104	Sequence 104, App
36	434	19.6	370	4	US-09-799-955-5	Sequence 5, Appli
37	434	19.6	370	4	US-09-461-436B-26	Sequence 26, Appl
38	434	19.6	370	4	US-09-576-290-21	Sequence 21, Appl
39	434	19.6	370	4	US-09-576-290-104	Sequence 104, App
40	434	19.6	381	1	US-08-192-288-2	Sequence 2, Appli
41	434	19.6	381	2	US-08-687-355A-2	Sequence 2, Appli
42	434	19.6	381	3	US-09-200-673-16	Sequence 16, Appl
43	434	19.6	381	4	US-09-407-367-2	Sequence 2, Appli
44	434	19.6	381	4	US-09-708-392-11	Sequence 11, Appl
45	432.5	19.5	370	3	US-09-172-353-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-479-128-2

; Sequence 2, Application US/09479128

; Patent No. 6319710

; GENERAL INFORMATION:

; APPLICANT: Berglind Ran Olafsdottir

; APPLICANT: Jeffrey Gulcher

; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE

; FILE REFERENCE: 2345.1005-001

; CURRENT APPLICATION NUMBER: US/09/479,128

; CURRENT FILING DATE: 2000-01-07

; PRIOR APPLICATION NUMBER: US 09/379,083

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo Sapiens
US-09-479-128-2

Query Match 100.0%; Score 2218; DB 3; Length 425;
Best Local Similarity 99.8%; Pred. No. 9.9e-193;
Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVLT SV 420
        ||||||||||||||||||||||||||||||||||||||||:|||||||
Db    361 LSGKFREQKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVLT SV 420

Qy    421 TTVLP 425
        |||||
Db    421 TTVLP 425
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RESULT 2

US-08-846-704-2

; Sequence 2, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-704-2

```

```

Query Match          99.8%; Score 2214; DB 3; Length 425;
Best Local Similarity 99.5%; Pred. No. 2.3e-192;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLV FALCYLPISVLNV LKRVFGMFRQASDREAVYACFTTFSHWL VYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVLVLV FALCYLPISVLNV LKRVFGMFRQASDREAVYACFTTFSHWL VYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420

```

```

Db          361 LSGKFREQFKAAFSCLPGLGPCSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420
Qy          421 TTVLP 425
          |||||
Db          421 TTVLP 425

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RESULT 3

US-09-211-823C-22

```

; Sequence 22, Application US/09211823C
; Patent No. 6664229
; GENERAL INFORMATION:
; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNETT, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-22

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```

Query Match          99.8%; Score 2214; DB 4; Length 425;
Best Local Similarity 99.5%; Pred. No. 2.3e-192;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy          61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy          121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy          181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

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QY 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

QY 301 MVLVLFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTTFSHWL VYANSAANPIIYNF 360
 |||
 Db 301 MVLVLFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTTFSHWL VYANSAANPIIYNF 360

QY 361 LSGKFREQFKA AFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 |||: |||
 Db 361 LSGKFREQFKA AFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

QY 421 TTVLP 425
 |||
 Db 421 TTVLP 425

RESULT 4

US-08-846-704-4

; Sequence 4, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,704

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-704-4

Query Match 95.0%; Score 2108; DB 3; Length 402;
Best Local Similarity 100.0%; Pred. No. 8.5e-183;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402
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RESULT 5

US-08-462-509B-2

; Sequence 2, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/462,509B
;   FILING DATE:  05-JUN-1995
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  WO PCT/US95/05616
;   FILING DATE:  05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Wales, Michele M.
;   REGISTRATION NUMBER:  43,975
;   REFERENCE/DOCKET NUMBER:  PF168P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  301-309-8504
;   TELEFAX:  301-309-8439
;   INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 402 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-462-509B-2

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Query Match          94.8%;  Score 2104;  DB 4;  Length 402;
Best Local Similarity 99.8%;  Pred. No. 2e-182;
Matches 401;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLV FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVLVLV FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKA AFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 LSGKFREQFKA AFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402

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RESULT 6

PCT-US95-05616-2

; Sequence 2, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-268

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN

PCT-US95-05616-2

Query Match 94.8%; Score 2104; DB 5; Length 402;

Best Local Similarity 99.8%; Pred. No. 2e-182;

Matches 401; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGBALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGBALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

```

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy      241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy      301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSGKFREQFKAASFCCPLGPGSLKAPSPRSSASHKSLSL 402
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 LSGKFREQFKAASFCCPLGPGSLKAPSPRSSASHKSLSL 402

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RESULT 7

US-08-846-705-2

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; Sequence 2, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: RATNER & PRESTIA
;     STREET: P.O. BOX 980
;     CITY: VALLEY FORGE
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19482
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/846,705
;     FILING DATE: 30-APR-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: PRESTIA, PAUL F
;     REGISTRATION NUMBER: 23,031
;     REFERENCE/DOCKET NUMBER: GH-70003
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 610-407-0700
;     TELEFAX: 610-407-0701
;     TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 389 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-705-2

Query Match 85.7%; Score 1902.5; DB 2; Length 389;
Best Local Similarity 96.1%; Pred. No. 3.3e-164;
Matches 368; Conservative 2; Mismatches 10; Indels 3; Gaps 2;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSAVLTLFSLALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSAVLTLFSLALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSC-CLPGLGP 382
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Db    361 LSG--CKEKSIALSCPCPGHDP 381
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RESULT 8

US-09-211-823C-23

; Sequence 23, Application US/09211823C

; Patent No. 6664229

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785
 ; PRIOR FILING DATE: 1997-12-16
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 389
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-211-823C-23

Query Match 85.7%; Score 1902.5; DB 4; Length 389;
 Best Local Similarity 96.1%; Pred. No. 3.3e-164;
 Matches 368; Conservative 2; Mismatches 10; Indels 3; Gaps 2;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRVRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSC-CLPGLGP 382
        |||  ::  |||  ||  |
Db    361 LSG--CKEKSLLALSCPCPGHDP 381
  
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RESULT 9

PCT-US95-05616-6

; Sequence 6, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

```

;      ZIP: 07068
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: 3.5 INCH DISKETTE
;      COMPUTER: IBM PS/2
;      OPERATING SYSTEM: MS-DOS
;      SOFTWARE: WORD PERFECT 5.1
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: PCT/US95/05616
;      FILING DATE: concurrently
;      CLASSIFICATION:
;      ATTORNEY/AGENT INFORMATION:
;      NAME: FERRARO, GREGORY D.
;      REGISTRATION NUMBER: 36,134
;      REFERENCE/DOCKET NUMBER: 325800-268
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 201-994-1700
;      TELEFAX: 201-994-1744
;      INFORMATION FOR SEQ ID NO: 6:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 377 BASE PAIRS
;      TYPE: AMINO ACID
;      STRANDEDNESS: SINGLE
;      TOPOLOGY: LINEAR
;      MOLECULE TYPE: cDNA
PCT-US95-05616-6

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Query Match          85.7%; Score 1901; DB 5; Length 377;
Best Local Similarity 96.6%; Pred. No. 4.4e-164;
Matches 366; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVLLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPG 379
      ||| : : || ||
Db    361 LSGCKEKS LVLSPSC--PG 377

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RESULT 10
 US-08-462-509B-4
 ; Sequence 4, Application US/08462509B
 ; Patent No. 6410701
 ; GENERAL INFORMATION:
 ; APPLICANT: Soppet, Daniel et al
 ; TITLE OF INVENTION: Human Neuropeptide Receptor
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,509B
 ; FILING DATE: 05-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US95/05616
 ; FILING DATE: 05-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wales, Michele M.
 ; REGISTRATION NUMBER: 43,975
 ; REFERENCE/DOCKET NUMBER: PF168P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-462-509B-4

Query Match 85.5%; Score 1897; DB 4; Length 369;
 Best Local Similarity 99.7%; Pred. No. 9.8e-164;
 Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDEFRLYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDEFRLYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

 Qy 121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLEKSTARRARGSLIGIWAIVSLAIMVPQA 180

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVQA 180

Qy      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy      241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSG 363
      |||
Db      361 LSG 363

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RESULT 11

PCT-US95-05616-4

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; Sequence 4, Application PC/TUS9505616
; GENERAL INFORMATION:
;   APPLICANT: LI, ET AL.
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;     ADDRESSEE: CECCHI, STEWART & OLSTEIN
;     STREET: 6 BECKER FARM ROAD
;     CITY: ROSELAND
;     STATE: NEW JERSEY
;     COUNTRY: USA
;     ZIP: 07068
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5 INCH DISKETTE
;     COMPUTER: IBM PS/2
;     OPERATING SYSTEM: MS-DOS
;     SOFTWARE: WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US95/05616
;     FILING DATE: concurrently
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: FERRARO, GREGORY D.
;     REGISTRATION NUMBER: 36,134
;     REFERENCE/DOCKET NUMBER: 325800-268
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 201-994-1700
;     TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 369 BASE PAIRS
;     TYPE: AMINO ACID
;     STRANDEDNESS: SINGLE
;     TOPOLOGY: LINEAR

```

; MOLECULE TYPE: cDNA
PCT-US95-05616-4

Query Match 85.5%; Score 1897; DB 5; Length 369;
Best Local Similarity 99.7%; Pred. No. 9.8e-164;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEQYEWVLIAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MCVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MCVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
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RESULT 12

US-08-462-509B-6

; Sequence 6, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/462,509B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05616
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-509B-6

```

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Query Match          85.4%; Score 1894; DB 4; Length 372;
Best Local Similarity 99.4%; Pred. No. 1.8e-163;
Matches 361; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGPVPPGSRDPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363

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RESULT 13
US-09-426-290-2
; Sequence 2, Application US/09426290

```

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; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-426-290-2
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Query Match          65.8%; Score 1460; DB 4; Length 444;
Best Local Similarity 68.8%; Pred. No. 4.6e-124;
Matches 284; Conservative 50; Mismatches 69; Indels 10; Gaps 5;
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```
Qy      17 SREPSVPDPDYED-EFLRYLWRDYLYPKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
          ::|| | ||:| |||||::||:|:||||| | : |||||:| | ||:|:|:|
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYQLQAVSVSVAVL 135
          |||||:|:|:|:| | ||:|:|:|:| | | :||| | | |||:| |
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYQLQTVSVSVSVL 143

Qy     136 TLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA AVMECSSVLPELANR 195
          || | |||||:|:|:|:| | | | | | | | | | | | | | | | | | |
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203

Qy     196 TRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
          | ||:| | | | :||:| | ||:|:|:| | | :| | | | | | | | | | | :
Db     204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCMLVLA YLQIFRKLWCRQIPGTSSVVQ 263

Qy     256 RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLLVFALCYLP 313
          | | | :| | | : | : | | |:|:| | | | | | | | | | | | | | | |
Db     264 RKWKPLQPV SQ----PRGPGQPTKS RMSAVAAEIKQIRARRKTARMLMVLLLVFAICYLP 319

Qy     314 ISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAF 373
          ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     320 ISILNVLKR VFGMFAHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKAAF 379

Qy     374 SCCLPGLGPCGSLKAPSPRSSA-SHKSLSLQ--SRC SVSKISEHVVLTSVTTV 423
          ||| |: : : | | | | | : : ||:| | | | | | | | | | | |
Db     380 SCCCLGVHHRQEDRLTRGRTSTESRKS LTTQISNFDNISKLSEQVVLTSISTL 432
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RESULT 14
US-09-119-788-2
; Sequence 2, Application US/09119788
; Patent No. 6166193
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
```

```

; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,788
; FILING DATE: 21-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-119-788-2

```

```

Query Match          65.8%; Score 1459; DB 3; Length 444;
Best Local Similarity 68.8%; Pred. No. 5.6e-124;
Matches 284; Conservative 50; Mismatches 69; Indels 10; Gaps 5;

```

```

Qy      17 SREPSVPDPDYED-EFLRYLWRDYLYPKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
      ::|| | ||:| |||||:|:|:|:|:|:| | | ||||:| | ||:|:| |
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGLHALCKVIPYLQAVSVSVAVL 135
      |||||:|:|:|:|:|:| | ||:|:|:|:| | | :||| | ||||:| |
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy     136 TLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA AVMECSSVLPELANR 195
      || | |||||:|:|:|:| | | : || | | ||:| | |||:| | |||:
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203

Qy     196 TRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
      | ||:|:| | :|:|:| | ||:|:|:| | | :|| ||||| ||||:| :
Db     204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

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; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-54

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Query Match          59.1%; Score 1311; DB 3; Length 263;
Best Local Similarity 96.6%; Pred. No. 7.5e-111;
Matches 254; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

```

```

Qy      91 ADVLVTAICLPASLLVDITESWLFGHALCKVIPYLAQAVSVSVAVLTLSFIALDRWYAICH 150
         |||||||
Db      1 ADVLVTAICLPASLLVDITESWLFGHALCKVIPYLAQAVSVSVVLTLSIALDRWYAICH 60

Qy     151 PLLFKSTARRARGSI LGIWA VSLAIMVPQA AVM ECSSVLPELANRTR LFSVC DERWADDL 210
         |||||||:|||||
Db      61 PLLFKSTARRARGSI LGIWA VSLAV MVPQA AVM ECSSVLPELANRTR LLSVC DERWADDL 120

Qy     211 YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQ 270
         |||||||
Db     121 YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLDDQGQ 180

Qy     271 GLSGEPQPRARAFLAEVKQMRARRKTAKMLMVVLLVFALCYLPISVLNVLKRVFGMFRQA 330
         ||| |||||||
Db     181 GLSSEPQPRARAFLAEVKQMRARRKTAKMLMVVLLVFALCYLPISVLNVLKRVFGMFRQA 240

Qy     331 SDREAVYACFTFSHWLVYANSAA 353
         |||||:|||||

```

Db 241 SDREAIYACFTFSHWLVYANSAA 263

Search completed: October 14, 2004, 10:58:11
Job time : 26.8791 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:42:40 ; Search time 22.5986 Seconds
(without alignments)
1809.496 Million cell updates/sec

Title: US-10-070-532-2
Perfect score: 2219
Sequence: 1 MEPSATPGAQMGVPPGSREP.....CSVSKISEHVVLTSVTTVLP 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	464.5	20.9	427	2	S50150	gastric CCK-A rece	
2	447.5	20.2	449	2	A41738	neuropeptide Y rec	
3	434	19.6	381	2	I39187	neuropeptide Y/pep	
4	432.5	19.5	370	1	I52315	G protein-coupled	
5	428.5	19.3	428	2	JN0692	cholecystokinin ty	
6	421.5	19.0	444	2	A42685	cholecystokinin re	
7	419	18.9	407	2	S23510	neurokinin 1 recep	
8	418	18.8	407	2	A34357	neurokinin 1 recep	
9	417.5	18.8	519	2	S17783	tachykinin recepto	
10	417	18.8	407	1	JQ1274	neurokinin 1 recep	
11	417	18.8	407	2	S20304	neurokinin 1 recep	
12	417	18.8	430	2	I51898	cholecystokinin A	
13	416	18.7	465	1	JQ1517	neurokinin 3 recep	

14	414.5	18.7	452	2	A34916	neurokinin 3 recep
15	413.5	18.6	402	2	I56595	neurokinin 2 recep
16	413	18.6	436	2	JC5599	cholecystokinin-A
17	409.5	18.5	452	2	JC2459	gastrin/cholecysto
18	408.5	18.4	385	2	S55524	neurokinin 3 recep
19	406.5	18.3	450	2	JQ1614	gastrin receptor -
20	403.5	18.2	398	1	JQ1059	neurokinin 2 recep
21	403.5	18.2	452	2	A46195	cholecystokinin B
22	403	18.2	384	1	S00516	neurokinin 2 recep
23	401	18.1	584	2	JC7809	sulfakinin recepto
24	400.5	18.0	423	2	B40470	glucocorticoid-ind
25	400.5	18.0	440	2	A44081	kappa-type opioid
26	399	18.0	447	2	A47430	gastrin/cholecysto
27	398	17.9	349	2	I59336	galanin receptor 1
28	397	17.9	384	2	I57957	neurokinin 2 recep
29	396	17.8	390	2	A36737	neurokinin 2 recep
30	394	17.8	453	2	S32817	gastrin receptor -
31	393.5	17.7	423	2	JC7677	allatostatin recep
32	389	17.5	504	2	A41783	tachykinin recepto
33	385.5	17.4	399	2	S29480	bombesin receptor
34	384	17.3	366	2	S71152	neuropeptide Y/pep
35	383.5	17.3	384	2	S20303	neurokinin 2 recep
36	382.5	17.2	443	2	D40470	glucocorticoid-ind
37	381.5	17.2	384	2	A39003	bombesin/gastrin-r
38	379	17.1	477	1	QRHUB1	beta-1-adrenergic
39	378.5	17.1	390	2	B41007	bombesin receptor,
40	378	17.0	394	2	JC7209	galanin receptor -
41	372.5	16.8	387	2	JC5949	galanin receptor 2
42	372.5	16.8	480	2	I53053	beta 1 adrenergic
43	368.5	16.6	375	2	S63685	neuropeptide Y rec
44	368.5	16.6	384	2	I57682	bombesin/ GRP rece
45	368.5	16.6	399	2	A46632	bombesin-like pept

ALIGNMENTS

RESULT 1

S50150

gastric CCK-A receptor - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000

C;Accession: S50150

R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.

Biochim. Biophys. Acta 1219, 321-327, 1994

A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.

A;Reference number: S50150; MUID:95002144; PMID:7918628

A;Accession: S50150

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-427 <REU>

C;Superfamily: neurokinin 1 receptor

Query Match 20.9%; Score 464.5; DB 2; Length 427;

Best Local Similarity 29.6%; Pred. No. 2.1e-31;

Matches 128; Conservative 85; Mismatches 168; Indels 51; Gaps 13;

Qy 8 GAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEQYEW---VLIAAYVAVFVVALVGN 64
| | : | | : | | : | | : | : : : | |
Db 9 GNASGIPP-----PCELGLDNETLFCLDQP---PPSKEWQPAVQILLYSLIFLLSVLGN 59

Qy 65 TLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPY 124
| | : | | | | | | : : : : : : | : | : : : : : | | | | |
Db 60 TLVITVLIRNKRMRVTNIFLLSLAISDLMLCLFCMPFNLPNLLKDFIFGSALCKTTTY 119

Qy 125 LQAVSVSVAVLTLSFIALDRWYAICHPLLFK--STARRARGSILGIWAVSLAIMVPQAAV 182
| | | : | | : : : | | | : | | | : | | | |
Db 120 LMGTSSVSSTLNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFAIMTPYPIY 179

Qy 183 MECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKL 242
| : : | : : | : : | : : : : : | : | : | : | : |
Db 180 ---SNLVPFCTKTNQTANMCRFLPSDVMQQAHTFLLLILFLIPGIVMMVAYGMISLEL 236

Qy 243 W-GRQIPGTTSALVRNWK-----RPSDQLGDLEQGLSGEPQPRARA 282
: | : : : | : : | : | : | | | |
Db 237 YQGIKFDASQKSAKERKASTGSGRFEDNDGCYLQRSKPTRQL-ELQQ-LSGGGGGRVSR 294

Qy 283 F--LAEVKQMRARRKTAKMLMVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACF 340
: : | : : : | | | : : | : : : : : : : : : :
Db 295 IHSSSSAAALMAKKRVIRMLMVIVVLFFLCWMPIFSANAWRAYDTV---SAERRLSGTPI 351

Qy 341 TFSHWLVYANSAANPIIYNFLSGKFREQFKAASFCCPLGLGPCGSLKAPSPRSSASHKSL 400
: | | : | | | | : : : | | | | | | | | | | : | :
Db 352 SFILLSTSSCVNPIIYCFMKNRFLGFMAFPCP-PNPGP-----PGPRAEAGEEEEE 404

Qy 401 SLQSRCSVSKIS 412
: | | : |
Db 405 GRTRASLSRYS 416

RESULT 2

A41738

neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: G protein-coupled receptor PR4

C;Species: *Drosophila melanogaster*

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: UNIPROT:P25931; GB:M81490; NID:g157996; PIDN:AAA28727.1; PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match

20.2%; Score 447.5; DB 2; Length 449;

Best Local Similarity 29.4%; Pred. No. 5.9e-30;
Matches 109; Conservative 63; Mismatches 138; Indels 61; Gaps 9;

```

Qy      26 DYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFI 85
      ||:  |  |  :: ::  |: |: | |:|  ||  |:  ||| |||
Db      75 DYD-----LLSEDMWSSAYFKIIVYMLYIPIFIFALIGNGTVCYIVYSTPRMRTVTNYFI 129

Qy      86 VNLSLADVLVTAICLPASLL-VDITESWLFGLHALCKVIPYLAQAVSVSAVLTLSFIALDR 144
      :|:: |:|:: | |:| : : |  || ||| : | |||| |:  ||  |::|
Db     130 ASLAIGDILMSFFCEPSSFISLFILNYWPFGLALCHFVNYSQAVSVLVSAYTLVAISIDR 189

Qy     145 WYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQAAMVMECSSVLPELANRTRLF SVCDE 204
      : ||  || : || |  ||:| ::|| :|  :  :  : :| |
Db     190 YIAIMWPLKPRITKRYATFIIAGVWFIALATALPIPIVSGLDIPMSPWHTKCEKY-ICRE 248

Qy     205 RWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQ 264
      |  |  | : :: |||:  | :| ::| :: |  :  ||
Db     249 MWPSRSQEYYYTSLFALQFVVPGLGVLIPTYARITIRVWAKRPPGEA-----ETNRDQ 301

Qy     265 LGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVF 324
      :  |:| | ||:| |:| | |:| ::| :|
Db     302 -----RMARSKRKMVKMMLTVVIVFTCCWLPFNILQLL----- 334

Qy     325 GMFRQASDREAV-----YACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAFS----- 374
      :| |  | | | ||| ::  |||| :: :| |
Db     335 -----LNDEEFHWDFLPYVWF AF-HWLAMSHCCYNPIIYCYMNARFRSGFVQLMHRMPG 388

Qy     375 ----CCLPGLG 381
      ||| :|
Db     389 LRRWCCLRSVG 399

```

RESULT 3

I39187

neuropeptide Y/peptide YY receptor Y2 - human

N;Alternate names: neuropeptide y/peptide YY receptor type 2

C;Species: Homo sapiens (man)

C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: I39187; I39163; G02301

R;Gerald, C.; Walker, M.W.; Vaysse, P.J.

J. Biol. Chem. 270, 26758-26761, 1995

A;Title: Expression cloning and pharmacological characterization of a human hippocampal neuropeptide Y/peptide YY Y2 receptor subtype.

A;Reference number: I39187; MUID:96070760; PMID:7592910

A;Accession: I39187

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-381 <GER>

A;Cross-references: UNIPROT:P49146; EMBL:U36269; NID:g1063633; PIDN:AAC50281.1; PID:g1063634

R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kienzle, B.; Seethala, R.

J. Biol. Chem. 270, 22661-22664, 1995

A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptide Y receptor.

A;Reference number: I39163; MUID:96032678; PMID:7559383

A;Accession: I39163

A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-133,'A',135-381 <ROS>
 A;Cross-references: EMBL:U32500; NID:g1000750; PIDN:AAA93170.1; PID:g1000751
 R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.;
 Karbon, W.
 submitted to the EMBL Data Library, December 1995
 A;Reference number: H01019
 A;Accession: G02301
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
 A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID:g1314330
 C;Genetics:
 A;Gene: GDB:NPY2R
 A;Cross-references: GDB:4365607; OMIM:162642
 A;Map position: 4q31-4q31
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein;
 thiolester bond; transmembrane protein
 F;49-76/Domain: transmembrane #status predicted <TM1>
 F;87-113/Domain: transmembrane #status predicted <TM2>
 F;166-186/Domain: transmembrane #status predicted <TM4>
 F;221-237/Domain: transmembrane #status predicted <TM5>
 F;269-291/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;123-203/Disulfide bonds: #status predicted
 F;342/Binding site: palmitate (Cys) (covalent) #status predicted
 F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.6%; Score 434; DB 2; Length 381;
 Best Local Similarity 27.6%; Pred. No. 6.8e-29;
 Matches 112; Conservative 74; Mismatches 140; Indels 80; Gaps 10;

Qy	3	PSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVALV	62
		:: : : : : : ::	
Db	24	PQTTPRGEL-----VPDPEPELI-----DSTKLIEVQVVLILAYCSIILLGVI	66
Qy	63	GNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHGHALCKVI	122
		: : : : : : : ::	
Db	67	GNSLVIHVVIKFSMRTVTNFFIANLAVADLLVNTLCLPFTLTYYTLMGWEKMGVPVLCHLV	126
Qy	123	PYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGI-WAVSLAIMVPQAA	181
		:: : :: : :: : : :	
Db	127	PYAQGLAVQVSTITLVIALDRHRCIVYHLESK-ISKRISFLIIGLAWGISALLASPLAI	185
Qy	182	VMECS--SVLPELANRTRLFVCDERWADD---LYPKIYHSCFFIVTYLAPLGLMAMAYF	236
		:: : : : : : : : : :::	
Db	186	FREYSLIEIIPDFE-----IVACTEKWPGEKSIYGTVYSLSSLLILYVLPGLIISFSYT	240
Qy	237	QIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKT	296
		: : :	
Db	241	RIWSKLNKHNHVSPPGA-----ANDHYHQRRQKT	266
Qy	297	AKMLMVLLVFALCYLPISVLNVLKRVFQGMFRQASDREAVYACFTFSHWLVYANSAANPI	356
		: :: : : : : : : :	
Db	267	TKMLVCVVVFAVSWLP---LHAFQLAVDIDSQVLDLKEYKLIFTVFHIIAMCSTFANPL	323

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JN0692; JN0590
R;de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.
Biochem. Biophys. Res. Commun. 194, 811-818, 1993
A;Title: Molecular cloning, functional expression and chromosomal localization
of the human cholecystokinin type A receptor.
A;Reference number: JN0692; MUID:93343941; PMID:8343165
A;Accession: JN0692
A;Molecule type: mRNA
A;Residues: 1-428 <DEW>
A;Cross-references: UNIPROT:P32238; GB:L19315; NID:g306595; PIDN:AAA02819.1;
PID:g306596
A;Experimental source: gallbladder
R;Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.
Biochem. Biophys. Res. Commun. 193, 204-211, 1993
A;Title: Molecular cloning and functional expression of the human gallbladder
cholecystokinin A receptor.
A;Reference number: JN0590; MUID:93277552; PMID:8503909
A;Accession: JN0590
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-428 <ULR>
A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491
A;Experimental source: gallbladder
C;Comment: This protein has diverse physiological roles in the gastrointestinal
system where it mediates pancreatic growth and enzyme secretion, smooth muscle
contraction of the gallbladder and stomach, and secretion from gastric mucosal
cells.
C;Genetics:
A;Gene: GDB:CCKAR
A;Cross-references: GDB:141927; OMIM:118444
A;Map position: 4pter-4qter
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
phosphoprotein; transmembrane protein
F;40-67/Domain: transmembrane #status predicted <TM1>
F;78-104/Domain: transmembrane #status predicted <TM2>
F;116-137/Domain: transmembrane #status predicted <TM3>
F;158-178/Domain: transmembrane #status predicted <TM4>
F;208-234/Domain: transmembrane #status predicted <TM5>
F;314-332/Domain: transmembrane #status predicted <TM6>
F;350-369/Domain: transmembrane #status predicted <TM7>
F;10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;245,249,260,290/Binding site: phosphate (Ser) (covalent) (by protein kinase C)
#status predicted
F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status
predicted

```

Qy      16 GSREPSVPPPDYEDFLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGNTLVCLAVW 72
      ||      |      |:| | | | | | : || | | | | :|:::| ||| | :
Db      11 GSNITPPCELGLENETLFCL--DQPRPSK-EWQPAVQILLYSLIFLLSVLGNTLVITVLI 67

Qy      73 RNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHGHALCKVIPYLOAVSVSV 132

```

	[: : : : : : : : : : : :	
Db	68 RNKRMRTVTNIFLLSLAVSDMLCLFCMPFNLPNLLKDFIFGSAVCKTTTYFMGTSVSV	127
Qy	133 AVLTLSFIALDRWYAICHPLLEFK--STARRARGSGILGIWAVSLAIMVPQAAMVECSSVLP	190
	: : : : : : ::	
Db	128 STFNLVAISLERYGAICKPLQSRVWQTSHALKVIAATWCLSFTIMTPYPIY---SNLVP	184
Qy	191 ELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLW-----	243
	: :: : : : : : : : : : :	
Db	185 FTKNNNQNTANMCREFLLPNDDVMQQSWHTFLLLILFLIPGIVMMVAYGLISLELYQGIIKFEA	244
Qy	244 -----GRQIPGTTSA-----LVRNWKRPSD-QLGDLEQGLSGEPQPRARAFLAEV	287
	: : : : : : : :	
Db	245 SQKKSARKERKPSTTSSGKYEDSDGCYLQKTRPPRKLELRQLSTGSSSRAN-RIRS-NSSA	302
Qy	288 QOMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLV	347
	: : :~ : : :~:~ :~ : ~::~ :	
Db	303 ANLMAKKRVIRMLIVIVLFLCWMPIFSANAWR---AYDTASAERRLSGTPISFILLLS	359
Qy	348 YANSAANPIIYNFLSGKFREQFAAFSCCLPGLGPCGSLKAPSRRSSASHKSLSLQSRC	407
	: :~ : :	
Db	360 YTSSCVNPPIICYFMNKRFRLGFMATFPCC-PNPGPPGARGEVGEEEEGGTTGASL-SRFS	417
Qy	408 VSKISEHV 415	
	:	
Db	418 YSHMSASV 425	

RESULT 6

cholecystokinin receptor type A - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text change 09-Jul-2004

R;Wank, S.A.; Harkins, R.; Jensen, R.T.; Shapira, H.; de Weerth, A.; Slattery, T.

A;Title: Purification, molecular cloning, and functional expression of the cholecystokinin receptor from rat pancreas.

A;Accession: A42685

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P30551; GB:M88096; NID:g203383; PIDN:AAA40899.1; PIP:g203384

A;Note: sequence extracted from NCBI backbone (NCBIN:93814, NCBIP:93815)

Biochem. Biophys. Res. Commun. 213, 958-966, 1995

A;Reference number: JC4225; MUID:95382845; PMID:7654260

A;Status: preliminary

A;Residues: 1-223 <TAK>

R;Mantamadiotis, T.; Baldwin, G.S.

Biochem. Biophys. Res. Commun. 201, 1382-1389, 1994

A;Title: The seventh transmembrane domain of gastrin/CCK receptors contributes to non-peptide antagonist binding.

A;Reference number: PC2213; MUID:94296413; PMID:8024583

A;Accession: PC2213

A;Status: preliminary

A;Molecule type: protein

A;Residues: 366-389 <MAN>

C;Comment: This G-protein-coupled receptor is present in the gastrointestinal system, vagus nerve and localized areas of the central nervous system. It mediates pancreatic growth and enzyme secretion, smooth muscle contraction of the gallbladder and stomach. It is capable of activating phospholipase C and stimulating transduction by increasing levels of diacylglycerol, inositol phosphate, and inducing the subsequent release of intracellular calcium.

C;Genetics:

A;Gene: CCKAR

A;Introns: 53/1; 137/1; 224/2; 267/1

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein

F;57-82/Domain: transmembrane #status predicted <TM1>

F;93-119/Domain: transmembrane #status predicted <TM2>

F;131-151/Domain: transmembrane #status predicted <TM3>

F;173-193/Domain: transmembrane #status predicted <TM4>

F;225-249/Domain: transmembrane #status predicted <TM5>

F;330-348/Domain: transmembrane #status predicted <TM6>

F;366-389/Domain: transmembrane #status predicted <TM7>

Query Match 19.0%; Score 421.5; DB 2; Length 444;

Best Local Similarity 28.1%; Pred. No. 9.1e-28;

Matches 120; Conservative 83; Mismatches 171; Indels 53; Gaps 12;

```
Qy      16 GSREPSVPVPDYEDFLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGNTLVCLAVW 72
      ||      |      |:| | | | | : ||      : | | :|:::|:| | | :
Db      26 GSNITPPCELGLENETLFLCL--DQPQPSK-EWQSALQILLYSIIFLLSVLGNTLVITVLI 82

Qy      73 RNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGLHALCKVIPYLQAVSVSV 132
      ||      ||||| |::|::|::|:: | :| :| : : : :|| | :| | | |||
Db      83 RNKRMRTVTNIFLLSLAVSDLMLCLFCMPFNLI PNLLKDFIFGSAVCKTTTYFMGTSVSV 142

Qy     133 AVLTLSFIALDRWYAICHPLLFK--STARRAGSILGIWAVSLAIMVPQAAVMECSSVLP 190
      : | | :|:|: ||| || : | | | | :| || | | :|:|
Db     143 STFNLVAISLERYGAICRPLQSRVWQTKSHALKVIAATWCLSFTIMTPYPIY---SNLVP 199

Qy     191 ELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLW-GRQIPG 249
      | : ::|      | : : : : : :| | :| :| | :|: | :
Db     200 FTKNNNQ TANMCRFLPSDAMQSWQTFLLLLIFLLPGIVMVVAYGLISLELYQGKIFDA 259

Qy     250 TTSALVRNWKRPD-----QLGDLEQGLSGEPQPRARAFIAE 286
      : : |::|      :| | | | | | : :
Db     260 SQKKSACE-KKPSTGSSTRYEDSDGCYLQKSRPPRKLELQQLSSGSGGSRLNRIRS-SSS 317

Qy     287 VKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWL 346
      : |::: |::|:|::| |::| | | : : : : :| | |
Db     318 AANLIAKKRVIRMLIVIVVLFLLCWMPIFSANAWRAYDTV---SAEKHLSGTPISFILL 374

Qy     347 VYANSAANPIIYNFLSGKFREQFKAAFCCLPGLGPCG-----SLKAPSPRSS 394
```



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Qy      333 REAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAFSCCLPGLGPCGSLKAPSPR 392
      : ||      ||  ::  |||||  | : :||  ||  ||  ||  | :
Db      283 IQQVYLAIM---WLAMSSTMYNPIIYCCLNDRFRLGFKHAFRCC-PFI----- 326

Qy      393 SSASHKSLSL-----QSRCSVSKISEHVVLTSVTTVL 424
      |:| : : | :      |:: || | :|  : |::||:
Db      327 SAADYEGLEMKSTRYFQTQGSVYKVSR--LETTISTVV 362

```

RESULT 8

A34357
neurokinin 1 receptor - rat
N;Alternate names: NK-1 receptor; substance P receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: A38692; A34357; A40089
R;Hershey, A.D.; Dykema, P.E.; Krause, J.E.
J. Biol. Chem. 266, 4366-4374, 1991
A;Title: Organization, structure, and expression of the gene encoding the rat substance P receptor.
A;Reference number: A38692; MUID:91154239; PMID:1705552
A;Accession: A38692
A;Molecule type: DNA
A;Residues: 1-407 <HER>
A;Cross-references: UNIPROT:P14600; GB:M34751
R;Yokota, Y.; Sasai, Y.; Tanaka, K.; Fujiwara, T.; Tsuchida, K.; Shigemoto, R.; Kakizuka, A.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 264, 17649-17652, 1989
A;Title: Molecular characterization of a functional cDNA for rat substance P receptor.
A;Reference number: A34357; MUID:90036822; PMID:2478537
A;Accession: A34357
A;Molecule type: mRNA
A;Residues: 1-407 <YOK>
A;Cross-references: GB:J05097; NID:g207051; PIDN:AAA42175.1; PID:g207052
R;Hershey, A.D.; Krause, J.E.
Science 247, 958-962, 1990
A;Title: Molecular characterization of a functional cDNA encoding the rat substance P receptor.
A;Reference number: A40089; MUID:90161991; PMID:2154852
A;Accession: A40089
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-74,'R',76-212,'A',214-407 <HE2>
A;Cross-references: GB:M31477
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

```

Query Match          18.8%;  Score 418;  DB 2;  Length 407;
Best Local Similarity 27.6%;  Pred. No. 1.6e-27;
Matches 112;  Conservative 69;  Mismatches 149;  Indels 76;  Gaps 8;

```

```

Qy      29 DEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNL 88
      ::|:: | : | :      ||| : | ::||| :|  : :  ||| ||||: |||
Db      23 NQFVQPTWQIVLW-----AAAYTVIVVTSVVGNVVVIWII LAHKRMRTVTNYFLVNL 74

```

Qy	89	SLADVLVTAICLPASLLVDITSLWFLGHALCKVIPYQLQAVSVSAVLTLSFIALDRWYAI	148
		: : : : : : : : : : : : : : :	
Db	75	AFAEACMAAFNTVVNFTYAVHNWVYYGLFYCKFHNFFPIAALFASIYSMTAVAFDRYMAI	134
Qy	149	CHPLLKFKSTARRAGSILGIWAVSLAIMVPQA-----AVMECSSVLPELANRTRLF	199
		: : : : : : : :	
Db	135	IHPLQPRLSATATKVVFIVWVLALLLAF PQGYSTTETMPSRVVCMIEWPEHPNRT---	191
Qy	200	SVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTLSALVRNWK	259
		: : : : : : :	
Db	192	-----YEKAYHICVTVLIYFLPLLVI GYAYTVVGITLWASEIPGDSSDRYH---	237
Qy	260	RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNV	319
		: : : : : : : :	
Db	238	-----EQVSAKRKVVKMMIVVCTFAICWLPHFHVFFL	269
Qy	320	LKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAFSCC-LP	378
		: : : : : :	
Db	270	LPYINPDLYLKKFIQQVYLA---SMWLAMSSTMYNPPIIYCCLNDRFRLGFKHAFRCCPFI	326
Qy	379	GLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKI SEHVVLTSVTTVL	424
		: : : : : : :	
Db	327	SAGDYEGLEMKSTR-----YLOTOSSVYKVSRL--LETTISTVV	362

Qy 42 PKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLP 101
 | :: : : :|| || :| | ||||| |||||: || :|:: :
 Db 104 -----WSIL--FGGMVIVATGGNLIVVWIVMTTKRMRTVTNYFIVNLSIADAMVSSLNVT 156

Qy 102 ASLLVDITESWLFGHALCKVIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRA 161
 : : | || ||: :: :|: :| || |::||: || || : : |
 Db 157 FNYYYMLDSDWPFGEFYCKLSQFIAMLSICASVFTLMAISIDRYVAIRPLQPRMSKRCN 216

Qy 162 RGSILGIWAVSLAIMVPOAAVMECSSV-LPELANRTRLFSVCDERWAD-----DLYPKIY 215
 || | | | : | : |::|| || | | :|
 Db 217 LAIAAVIWLASTLISCPMMIIRTEEVPRGLSNRT-----VCYPEWPDGPTNHSTMESLY 272

Qy 216 HSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTALVRNWKRPDQLGDLEQGLSGE 275
 : |::|| |: | : | :: :||| : ||
 Db 273 NILIIILTYFLPIVSMTVTYSRVGIELWGSK-----TIGE 307

Qy 276 PQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREA 335
 || :|: :|::|: ||::||:|:|:|:|:| : : :| :
 Db 308 CTPR-----QVENVRSKRRVVKMMIVVLIFAICWLPFHSYFIITSCYPAITEAPFIQE 361

Qy 336 VYACFTFSHWLVYANSAANPIIYNFLSGKFREQKAAFSCCL 377
 :| :|| :|| |||| :: :|| || | ||
 Db 362 LYLAI---YWLAMNSMYNPPIIYCWMSRFRYGFKMVERWCL 400

RESULT 10

JQ1274

neurokinin 1 receptor - human

N;Alternate names: NK-1 receptor; substance P receptor

C;Species: Homo sapiens (man)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: A41134; JQ1274; JH0478; S21188

R;Gerard, N.P.; Garraway, L.A.; Eddy Jr., R.L.; Shows, T.B.; Iijima, H.; Paquet, J.L.; Gerard, C.

Biochemistry 30, 10640-10646, 1991

A;Title: Human substance P receptor (NK-1): organization of the gene, chromosome localization, and functional expression of cDNA clones.

A;Reference number: A41134; MUID:92031510; PMID:1657150

A;Accession: A41134

A;Molecule type: DNA

A;Residues: 1-328, 'G', 329-332, 334-407 <GER>

A;Cross-references: UNIPROT:P25103; GB:M76675; NID:g189231

A;Note: in the authors' translation 333-Gly is shown before residue 329 and, consequently, residues 329-332 are displaced one codon to the right

R;Takeda, Y.; Chou, K.B.; Takeda, J.; Sachais, B.S.; Krause, J.E.

Biochem. Biophys. Res. Commun. 179, 1232-1240, 1991

A;Title: Molecular cloning, structural characterization and functional expression of the human substance P receptor.

A;Reference number: JQ1274; MUID:92028856; PMID:1718267

A;Accession: JQ1274

A;Molecule type: mRNA

A;Residues: 1-407 <TAK1>

A;Cross-references: GB:M74290; NID:g338612; PIDN:AAA60601.1; PID:g338613

R;Hopkins, B.; Powell, S.J.; Danks, P.; Briggs, I.; Graham, A.

Biochem. Biophys. Res. Commun. 180, 1110-1117, 1991

A;Title: Isolation and characterization of the human lung NK-1 receptor cDNA.

A;Reference number: JH0478; MUID:92062052; PMID:1659396
 A;Accession: JH0478
 A;Molecule type: mRNA
 A;Residues: 1-407 <HOP>
 A;Cross-references: GB:S62045; NID:g237994; PIDN:AAB20168.1; PID:g237995
 A;Experimental source: lung
 A;Note: the authors translated the codon CAA for residue 31 as Glu
 R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
 Eur. J. Biochem. 204, 1025-1033, 1992
 A;Title: The primary structure and gene organization of human substance P and
 neuromedin K receptors.
 A;Reference number: S21188; MUID:92201186; PMID:1312928
 A;Accession: S21188
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-407 <TAK2>
 A;Cross-references: GB:X65177; NID:g36636; PIDN:CAA46292.1; PID:g825721
 C;Comment: The endogenous ligand of this receptor is neurokinin 1 (substance P),
 one of the peptides in the mammalian tachykinin system.
 C;Genetics:
 A;Gene: GDB:TAC1R
 A;Cross-references: GDB:128977; OMIM:162323
 A;Map position: 2pter-2qter
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
 transmembrane protein
 F;32-58/Domain: transmembrane #status predicted <TM1>
 F;69-92/Domain: transmembrane #status predicted <TM2>
 F;110-128/Domain: transmembrane #status predicted <TM3>
 F;149-168/Domain: transmembrane #status predicted <TM4>
 F;195-221/Domain: transmembrane #status predicted <TM5>
 F;249-273/Domain: transmembrane #status predicted <TM6>
 F;286-308/Domain: transmembrane #status predicted <TM7>
 F;14,18/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;105-180/Disulfide bonds: #status predicted

Query Match 18.8%; Score 417; DB 1; Length 407;
 Best Local Similarity 28.0%; Pred. No. 2e-27;
 Matches 110; Conservative 69; Mismatches 152; Indels 62; Gaps 10;

Qy	42	PKQY---EWVLI---AAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLV	95
		: : : : : : : : : : :	
Db	22	PNQFVQPAWQIVLWAAAYTVIVVTSVVGNVVVMWII LAHKRMRTVTNYFLVNLAF AEASM	81
Qy	96	TAICLPASLLVDITESWLF GHALCKVIPY LQAVSVSVAVLTLSFIALDRWYAICHPLLFK	155
		: : : : : : : : : : : : :	
Db	82	AAFNTVVNFTYAVHNEWYYGLFYCKFHNF FPIAAVFASIYSMTAVAFDRYMAIIHPLQPR	141
Qy	156	STARRARGSILGIWAVSLAIMVPQAAVMECSSLPELANRTRLFSVC DERWAD---DIYP	212
		: : : : : : : : : : : :	
Db	142	LSATATKVVICVIWVLALLLAF PQGY---STTETMP SRV---VCMIEWPEHPNKIYE	193
Qy	213	KIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRP SDQLGDLEQGL	272
		: : : : : : : :	
Db	194	KVYHICVTVLIYFLPLLIVIGYAYTVVGITLWASEIPGDSSDRYH-----	237
Qy	273	SGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKR VFGMFRQASD	332

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      ::|:|:| |::|:| |::|:| : :| :
Db      238 -----EQVSARKRVKMMIVVCTFAICWLPFHIFLLPYINPDLYLKKF 282
Qy      333 REAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQKAAFSCC-LPGLGPCGSLKAPSP 391
      : ||      || ::| |::| |: :|| || || | | : |
Db      283 IQQVYLAIM---WLAMSSTMYNPPIIYCCLNDRFRLGFKHAFRCCPFISAGDYEGLEMKST 339
Qy      392 RSSASHKSLSLQSRCSVSKISEHVVLTSVTTVL 424
      |      |::| | |:| : |::|:|:
Db      340 R-----YLQTQGSVYKVSRL--LETTISTVV 362

```

RESULT 11

S20304

neurokinin 1 receptor - mouse

N;Alternate names: NK-1 receptor; substance P receptor

C;Species: Mus musculus (house mouse)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S20304; I56216; I73044

R;Sundelin, J.B.; Provvedini, D.M.; Wahlestedt, C.R.; Laurell, H.; Pohl, J.S.; Peterson, P.A.

Eur. J. Biochem. 203, 625-631, 1992

A;Title: Molecular cloning of the murine substance K and substance P receptor genes.

A;Reference number: S20303; MUID:92137253; PMID:1370937

A;Accession: S20304

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-407 <SUN>

A;Cross-references: UNIPROT:P30548; GB:X62934; NID:g54206; PIDN:CAA44707.1; PID:g54207

R;Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.

J. Immunol. 152, 1830-1835, 1994

A;Title: Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansoni express an authentic substance P (NK-1) receptor.

A;Reference number: I56216; MUID:94165478; PMID:8120392

A;Accession: I56216

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 63-290 <COO1>

A;Cross-references: GB:L27826; NID:g450286; PIDN:AAA17891.1; PID:g480776

A;Experimental source: tissue brain

A;Accession: I73044

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 63-290 <COO2>

A;Cross-references: GB:L27828; NID:g450290; PIDN:AAA17892.1; PID:g480778

A;Experimental source: tissue granuloma

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.8%; Score 417; DB 2; Length 407;

Best Local Similarity 27.3%; Pred. No. 2e-27;

Matches 111; Conservative 70; Mismatches 149; Indels 76; Gaps 8;

Qy 29 DEFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNL 88

```

Db      23 NQFVQPTWQIVLW-----AAAYTVIVVTSVVGNNVVIWIILAHKRMRTVTNYFLVNL 74
Qy      89 SLADVLVTAICLPASLLVDITESWLFEGHALCKVIPYQLQAVSVSVAVLTLSFIALDRWYAI 148
      : | : : | : : | : | : : : : : : : : : : : : : :
Db      75 AFAEACMAAFNTVNFYAVHNVWYGYGLEYCKFHNFFPIAALFASIYSMTAVAFDRYMAI 134
Qy     149 CHPLLFKSTARRARGSI LGIWA VSLAIMVPQA-----AVMECSSVLPELANRTRLF 199
      ||| : : | : | || : : | || : : | || ||
Db     135 IHPLQPRLSATATKVVFVIVWLALLLAFPGQGYSTTETMPSRVVCMIIEWPEHPNRT--- 191
Qy     200 SVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWK 259
      | | | | : : | | : : | | : : | | : : | |
Db     192 -----YEKAYHICVTVLIYFLPLLVI GYAYTVVGITLWASEIPGDSSDRYH--- 237
Qy     260 RPSDQLGDLEQGLSGEPQPRARAFIAEVKQMRARRKTAKMLMVLLLVFALCYLPISVLNV 319
      : | : | | | : : | | : : | | : :
Db     238 -----EQVSAKRKVVKMMIVVCTFAICWLPFHIFFL 269
Qy     320 LKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQKAAFSCC-LP 378
      | : : | | : : | | | | : : | | | | | |
Db     270 LPYINPDLYLKKFIQQVYLA---SMWLAMSSTMYNPIIYCCLNDRFRLGFKHAFRCCPFI 326
Qy     379 GLGPCGSLKAPSPRSSASHKSLQSRCSVSKISEHVVLTSVTTVL 424
      | | : | | | : : | | : : | : : | :
Db     327 SAGDYEGLEMKSTR-----YLQTQSSVYKVS R--LETTISTVV 362

```

RESULT 12

I51898

cholecystokinin A receptor - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004

C;Accession: I51898

R;De Weerth, A.; Pisegna, J.R.; Wank, S.A.

Am. J. Physiol. 265, G1116-G1121, 1993

A;Title: Guinea pig gallbladder and pancreas possess identical CCK-A receptor subtypes: receptor cloning and expression.

A;Reference number: I51898; MUID:94106629; PMID:7916580

A;Accession: I51898

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-430 <RES>

A;Cross-references: UNIPROT:Q63931; GB:S68242; NID:g544723; PIDN:AAB29504.1; PID:g544724

C;Superfamily: neurokinin 1 receptor

Query Match 18.8%; Score 417; DB 2; Length 430;

Best Local Similarity 28.4%; Pred. No. 2.1e-27;

Matches 122; Conservative 81; Mismatches 169; Indels 58; Gaps 13;

```

Qy      16 GSREPSVPVPDYEDFLRYLWRDYLYPK-QYEW---VLIAAYVAVFVVALVGNTLVCLAV 71
      || | : : | | | : | | | | : : : : | | | :
Db      11 GSNITSACELGFENETLFC LDR----PRPSKEWQPAVQILLYSLIFLLSVLGNLT LVITVL 66
Qy      72 WRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCKVIPYQLQAVSVS 131
      || | | | | | : : : : : : : : : : : : : : | | |

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R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
 Eur. J. Biochem. 204, 1025-1033, 1992
 A;Title: The primary structure and gene organization of human substance P and
 neuromedin K receptors.
 A;Reference number: S21188; MUID:92201186; PMID:1312928
 A;Accession: S21237
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-438, 'F', 440-465 <TAK>
 A;Cross-references: GB:X65172; NID:g35022; PIDN:CAA46291.1; PID:g825695
 C;Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromedin
 K), one of the peptides in the mammalian tachykinin system.
 C;Genetics:
 A;Gene: GDB:TACR3
 A;Cross-references: GDB:9599126
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
 transmembrane protein
 F;83-111/Domain: transmembrane #status predicted <TM1>
 F;122-147/Domain: transmembrane #status predicted <TM2>
 F;160-181/Domain: transmembrane #status predicted <TM3>
 F;202-221/Domain: transmembrane #status predicted <TM4>
 F;247-272/Domain: transmembrane #status predicted <TM5>
 F;300-321/Domain: transmembrane #status predicted <TM6>
 F;333-355/Domain: transmembrane #status predicted <TM7>
 F;23,50,73/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;158-233/Disulfide bonds: #status predicted

Query Match 18.7%; Score 416; DB 1; Length 465;
 Best Local Similarity 28.7%; Pred. No. 2.8e-27;
 Matches 108; Conservative 70; Mismatches 142; Indels 56; Gaps 10;

Qy	4	SATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVALVG	63
		:: :: : :::: ::	
Db	52	SSSPSA-LGLPVASPPSQPWANLTNQFVQPSWRIAL-----WSL--AYGVVVAVAVLG	102
Qy	64	NTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFEGHALCKVIP	123
		: : : :: : : : : : :	
Db	103	NLIVIWIILAHKRMRTVTNYFLVNLAFSASMAAFNTLVNFIYALHSEWYFGANYCRFQN	162
Qy	124	YLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQAAM	183
		: : :::: :: : : : : :: :	
Db	163	FFPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQCLYS	222
Qy	184	ECSSVLPELANRTRLFSVCDERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		: : :: : : : : : :	
Db	223	K-TKVMP---GRT----LCFVQWPEG--PKQHFTYHIIVIIIVYCFPLLIMGITYTIVGI	272
Qy	241	KLWGRQIPGTTISALVRNWKRPSPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
		: : :: :	
Db	273	TLWGGEIPGDTCDKYH-----EQLKAKRKVVVKMM	301
Qy	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
		:::: :: : : : : : : ::	
Db	302	IIVVMTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLA---SFWLAMSSTMYNPIIYCC	358
Qy	361	LSGKFREQFKAAFSCC	376

Db 359 LNKRFERAGEFKRAFRWC 374

RESULT 14

neurokinin 3 receptor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: A34916

J. Biol. Chem. 265, 623-628, 1990

A;Reference number: A34916; MUID:90110113; PMID:2153106

A;Molecule type: mRNA

A;Cross-references: UNIPROT:P16177; GB:J05189; NID:g205670; PIDN:AAA41688.1;

C;Superfamily: neurokinin 1 receptor

Query Match 18.7%; Score 414.5; DB 2; Length 452;
Best Local Similarity 28.7%; Pred. No. 3.6e-27;
Matches 106; Conservative 66; Mismatches 142; Indels 55; Gaps 8;

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Qy      11  MGVPFGSREPSVPPDYEDEFRLRYLWRDYLYPEKQYEWVLLIAAYVAVFVVALVGNLTVCCLA 70
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Db      45  LGLPATTQAPSQVRANLTNQFVQPSWRIAL-----WSL--AYGLVVAVAVFGNLIWIWI 96

Qy      71  VWRNHMRTVTNRYFIVNLSLADVLTVAICLPASLLVDITESWLFGHALCKVIPYQLQAVSV 130
      :  :  |||||:|:|:|  | |  :  :  :  | ||  |:  :  :|
Db      97  ILAKHRMRTVTNRYFLVNLAFSDASVAAFNTLINFIYGLHSEWYFGANYCRFQNFPPITAV 156

Qy     131  SVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSI LGIWA VSLAIMVPQAAVMECSSVLP 190
      :: ::|:|:|  ||  ||  : :|  :  |  || ::  :  ||  | :
Db     157  FASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPOCLY----SKIK 212

Qy     191  ELANRTRLFSVCDERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQI 247
      :  ||  :|  :|  :  ||  ||  |:  |  || :|  :  :  ||| :|
Db     213  VMPGRT----LCYVQWPEG--PKQHFTYHIIIVIIILVYCFLLIMGVTYTIVGITLWGGEI 266

Qy     248  PGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVVLLVF 307
      || |  :|:|:|  |||  ||:|:|  |
Db     267  PGDTCDKYH-----EQLKAKRKVKMMIIVVVTF 295

Qy     308  ALCYLPISVLNVLKRVFQMFQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFRE 367
      |:|:|  |  :|  ::  :  :  ||  | ||  ::|  ||||  |:  :|
Db     296  AICWLPHYVYFILTAIYQQLNRWKYIQQVYLA---SFWLAMSSMTYNPIIYCCLNKRFR 352

Qy     368  QFKAASFCC 376
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Db     353  GFKRAFRWC 361

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RESULT 15

I56595
neurokinin 2 receptor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: I56595
R;Aharony, D.; Little, J.; Thomas, C.; Powell, S.; Downey-Jones, M.; Graham, A.
J. Recept. Res. 14, 399-421, 1994
A;Title: Isolation and characterization of neurokinin A receptor cDNAs from
guinea-pig lung and rabbit pulmonary artery.
A;Reference number: I56595; MUID:95182423; PMID:7877137
A;Accession: I56595
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-402 <RES>
A;Cross-references: UNIPROT:Q64077; GB:S76253; NID:g913274; PIDN:AAB33553.1;
PID:g913275
C;Superfamily: neurokinin 1 receptor

Query Match 18.6%; Score 413.5; DB 2; Length 402;
Best Local Similarity 29.7%; Pred. No. 3.9e-27;
Matches 113; Conservative 64; Mismatches 134; Indels 69; Gaps 12;

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Qy      47 WVL---IAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAS 103
      | |      ||::: ||: || | : : | ||||| ||||: ||: : | :
Db      31 WQLALWATAYLALVLVAVTGNATVTWII LAHQRMRTVTNYFIVNLALADLCMAAFNAAFN 90

Qy     104 LLVDITESWLFGHALCKVIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARG 163
      :      | || | | : : : ||: ||: || || : : | :
Db      91 FVYASHNIWYFGRAFCYFQNLFPITAMFVSIYSMTAIAIDRYMAIVHPFPQRLSAPSTKA 150

Qy     164 SILGIWAVSLAIMVPPQAAVMECSSVLPELANRTRLFVCDERWADDLYPK---IYHSCFF 220
      | || | ||: ||: || | : | : | : | : | : | : | :
Db     151 VIGGIWLVALALAFPQCFY----STITEDEGATK----CVVAWPEDSRDKSLLLYHLVVI 202

Qy     221 IVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSAIVRNWKRPSDQLGDLEQGLSGEPQPRA 280
      :: || || : | : || | || | : : : : : : : : : : ||
Db     203 VLIYLLPLTVMFVAYSII GLTLWRRV-----PRH 232

Qy     281 RAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQASDREAVYACF 340
      : | | : : : ||: | : : : ||: ||: | : : | : | : | :
Db     233 QAHGANLRHLQAKKKFVKTMVLVVVTF AICWLPYHLYFIL-----GSFQEDIY-CH 282

Qy     341 TFSH-----WLVYANSAANPIIYNFLSGKFREQKAAAFSCCLPGLGPCGLKAPSPRS 393
      | : : : || || | : : || | : || || | : | : : :
Db     283 KFIQQVYLALFWLAMSSTMYNPIIYCCLNRRFRSGFRLAFRCC-PWVTP-----TEEDKL 336

Qy     394 SASH-KSLSLQ-SRCSVSKI 411
      : | | ||: ||: : | :
Db     337 ELTHTPSFSLRVNRCHTKEI 356

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Search completed: October 14, 2004, 10:56:54
Job time : 23.5986 secs

OM protein - protein search, using sw model

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Run on:      October 14, 2004, 10:55:56 ; Search time 79.0952 Seconds
              (without alignments)
              1737.280 Million cell updates/sec
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Title: US-10-070-532-2
Perfect score: 2219
Sequence: 1 MEPSATPGAOMGVPPGSREP.....CSVSKISEHVVLTSVTTVLP 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Published Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query
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No.	Score	Match Length	DB	ID	Description
1	2218	100.0	425	9 US-09-961-848-2	Sequence 2, Appli
2	2215	99.8	425	9 US-09-828-538-24	Sequence 24, Appl
3	2214	99.8	425	9 US-09-828-538-19	Sequence 19, Appl
4	2214	99.8	425	10 US-09-211-823C-22	Sequence 22, Appl
5	2214	99.8	425	14 US-10-225-567A-368	Sequence 368, App
6	2214	99.8	425	14 US-10-352-684A-22	Sequence 22, Appl
7	2209	99.5	425	10 US-09-826-509-549	Sequence 549, App
8	2108	95.0	402	13 US-10-077-874-2	Sequence 2, Appli
9	2087	94.1	402	10 US-09-393-696-2	Sequence 2, Appli
10	2087	94.1	427	9 US-09-730-931-2	Sequence 2, Appli
11	1902.5	85.7	389	9 US-09-828-538-20	Sequence 20, Appl
12	1902.5	85.7	389	10 US-09-211-823C-23	Sequence 23, Appl
13	1897	85.5	369	13 US-10-077-874-4	Sequence 4, Appli
14	1894	85.4	372	10 US-09-393-696-6	Sequence 6, Appli
15	1894	85.4	372	13 US-10-077-874-6	Sequence 6, Appli
16	1869	84.2	369	10 US-09-393-696-4	Sequence 4, Appli
17	1474.5	66.4	460	14 US-10-081-810-46	Sequence 46, Appl
18	1460	65.8	444	10 US-09-992-331-19	Sequence 19, Appl
19	1460	65.8	444	14 US-10-081-810-45	Sequence 45, Appl
20	1460	65.8	444	14 US-10-225-567A-370	Sequence 370, App
21	1460	65.8	444	14 US-10-262-313-19	Sequence 19, Appl
22	1460	65.8	444	14 US-10-060-369-11	Sequence 11, Appl
23	1460	65.8	444	14 US-10-178-194-2	Sequence 2, Appli
24	1460	65.8	444	16 US-10-768-878-19	Sequence 19, Appl
25	1459	65.8	444	14 US-10-282-717-2	Sequence 2, Appli
26	1455	65.6	444	10 US-09-826-509-551	Sequence 551, App
27	1311	59.1	263	14 US-10-278-087A-54	Sequence 54, Appl
28	522.5	23.5	430	9 US-09-866-248A-8	Sequence 8, Appli
29	522.5	23.5	430	14 US-10-225-567A-658	Sequence 658, App
30	522.5	23.5	430	16 US-10-719-587-54	Sequence 54, Appl
31	522.5	23.5	441	14 US-10-292-798-890	Sequence 890, App
32	519.5	23.4	428	9 US-09-292-973-4	Sequence 4, Appli
33	507.5	22.9	432	9 US-09-866-248A-2	Sequence 2, Appli
34	507.5	22.9	432	16 US-10-719-587-37	Sequence 37, Appl
35	499.5	22.5	420	9 US-09-866-248A-6	Sequence 6, Appli
36	499.5	22.5	420	14 US-10-060-369-9	Sequence 9, Appli
37	499.5	22.5	522	14 US-10-081-810-53	Sequence 53, Appl
38	499.5	22.5	522	14 US-10-225-567A-512	Sequence 512, App
39	499.5	22.5	522	14 US-10-255-551-2	Sequence 2, Appli
40	499.5	22.5	522	15 US-10-072-012-360	Sequence 360, App
41	499.5	22.5	522	15 US-10-072-012-361	Sequence 361, App
42	499.5	22.5	522	15 US-10-276-774-2093	Sequence 2093, Ap
43	499.5	22.5	522	17 US-10-757-262-8	Sequence 8, Appli
44	499	22.5	417	15 US-10-072-012-358	Sequence 358, App
45	480	21.6	426	9 US-09-292-973-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-961-848-2

; Sequence 2, Application US/09961848

; Patent No. US20020146719A1

; GENERAL INFORMATION:

; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-004
; CURRENT APPLICATION NUMBER: US/09/961,848
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/479,128
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-961-848-2

Query Match 100.0%; Score 2218; DB 9; Length 425;
Best Local Similarity 99.8%; Pred. No. 5.8e-204;
Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGBHALCK 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGBHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVLVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
          ||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db    361 LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy    421 TTVLP 425
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Db    421 TTVLP 425
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RESULT 2
US-09-828-538-24

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; Sequence 24, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-24
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Qy	1	MEPSATPGAQMGVPPGSPVPPDYDEFLRYLRWDYLYPKQYEWVLIAYVAVFVVA	60
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Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Qy	121	VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWAVSLAIMVPOA	180
Db	121	VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWAVSLAIMVPOA	180
Qy	181	AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSGKFREQFKAASFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVLTSTV	420

Db 361 LSGKFREQFKAAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
Qy 421 TTVLP 425
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Db 421 TTVLP 425

RESULT 3

US-09-828-538-19

; Sequence 19, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-19

Query Match 99.8%; Score 2214; DB 9; Length 425;
Best Local Similarity 99.5%; Pred. No. 1.4e-203;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
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Db 61 LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARG SILGIWAVSLAIMVPQA 180
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Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARG SILGIWAVSLAIMVPQA 180

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Db      301 MIVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
Db      361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420
Qy      421 TTVLP 425
Db      421 TTVLP 425

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RESULT 4

US-09-211-823C-22

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; Sequence 22, Application US/09211823C
; Publication No. US20030087801A1
; GENERAL INFORMATION:
; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNETT, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-22

```

```

Query Match          99.8%; Score 2214; DB 10; Length 425;
Best Local Similarity 99.5%; Pred. No. 1.4e-203;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

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Qy      1 MEPSATPGAQMGPVPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db      1 MEPSATPGAQMGPVPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Qy      61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Db      61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

```

Qy 121 VIPYLQAVSVSAVLTLTSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPGA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 VIPYLQAVSVSAVLTLTSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPGA 180

Qy 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 ||||||||||||||||||||||||||||||||||||||||||||:||||||||||
 Db 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy 421 TTVLP 425
 |||||
 Db 421 TTVLP 425

RESULT 5

US-10-225-567A-368

; Sequence 368, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenna C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 368

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-368

Query Match 99.8%; Score 2214; DB 14; Length 425;
 Best Local Similarity 99.5%; Pred. No. 1.4e-203;
 Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAYVAVFVVA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSIILGIWAVSLAIMVPQA 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSIILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 ||||||||||||||||||||||||||||||||||||||||||||:||||||
 Db 361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy 421 TTVLP 425
 |||||
 Db 421 TTVLP 425

RESULT 6

US-10-352-684A-22

; Sequence 22, Application US/10352684A

; Publication No. US20030215452A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; APPLICANT: Weich, Nadine S.

; APPLICANT: Kelly, Louise M.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,

; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,

; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,

; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES

; FILE REFERENCE: MPI02-019P1RNOMNIM

; CURRENT APPLICATION NUMBER: US/10/352,684A

; CURRENT FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/354,333

; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: US 60/360,258

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/364,476

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: US 60/375,626

```

; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-352-684A-22

```

```

Query Match          99.8%; Score 2214; DB 14; Length 425;
Best Local Similarity 99.5%; Pred. No. 1.4e-203;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEWVLIAAYVAVFVVA 60
        |
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
        |
Db     61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        |
Db    121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |
Db    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        |
Db    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
        |
Db    361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy    421 TTVLP 425
        |
Db    421 TTVLP 425

```

RESULT 7

US-09-826-509-549

; Sequence 549, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 549

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-549

Query Match 99.5%; Score 2209; DB 10; Length 425;

Best Local Similarity 99.3%; Pred. No. 4.3e-203;

Matches 422; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSEFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSEFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTKKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSCLPLGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420

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          ||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db      361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy      421 TTVLP 425
          |||||
Db      421 TTVLP 425

```

RESULT 8

US-10-077-874-2

```

; Sequence 2, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;     APPLICANT: Soppet, Daniel et al
;     TITLE OF INVENTION: Human Neuropeptide Receptor
;     NUMBER OF SEQUENCES: 12
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Human Genome Sciences, Inc.
;       STREET: 9410 Key West Avenue
;       CITY: Rockville
;       STATE: MD
;       COUNTRY: USA
;       ZIP: 20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/077,874
;       FILING DATE: 20-Feb-2002
;       CLASSIFICATION: <Unknown>
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/462,509
;       FILING DATE: 05-JUNE-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Wales, Michele M.
;       REGISTRATION NUMBER: 43,975
;       REFERENCE/DOCKET NUMBER: PF168P1D1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 301-309-8504
;       TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 402 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

US-10-077-874-2

```

Query Match          95.0%; Score 2108; DB 13; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.9e-193;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPEPSVPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFVVA 60
          ||||||||||||||||||||||||||||||||||||||||||||

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```

Db          1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEWVLIAYVAVFVVA 60
QY          61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
            |
Db          61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
QY          121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180
            |
Db          121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180
QY          181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
            |
Db          181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
QY          241 KLWGRQIPGTTSALVRNWKRPDQDLEQGLSGEPQPRARAFIAEVKQMRARRKTAKML 300
            |
Db          241 KLWGRQIPGTTSALVRNWKRPDQDLEQGLSGEPQPRARAFIAEVKQMRARRKTAKML 300
QY          301 MVLVLFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
            |
Db          301 MVLVLFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
QY          361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402
            |
Db          361 LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402

```

RESULT 9

US-09-393-696-2

; Sequence 2, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; FILE REFERENCE: PF168P2

; CURRENT APPLICATION NUMBER: US/09/393,696

; CURRENT FILING DATE: 1999-09-10

; EARLIER APPLICATION NUMBER: PCT/US95/05616

; EARLIER FILING DATE: 1995-05-05

; EARLIER APPLICATION NUMBER: US08/462,509

; EARLIER FILING DATE: 1995-06-05

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 402

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-393-696-2

Query Match 94.1%; Score 2087; DB 10; Length 402;

Best Local Similarity 99.0%; Pred. No. 2e-191;

Matches 398; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY          1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEWVLIAYVAVFVVA 60
            |
Db          1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEWVLIIPAYVAVFVVA 60

```

Qy 61 LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
 |||
 Db 61 LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARG SILGIWAVSLAIMVPQA 180
 |||
 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARG SILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 NLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQFKA AFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402
 |||
 Db 361 LSGKFREQFKA AFSCCLPGLGPCGSLKAPSPRSSASHKSLSL 402

RESULT 10

US-09-730-931-2

; Sequence 2, Application US/09730931

; Patent No. US20020064814A1

; GENERAL INFORMATION:

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: DOG OREXIN 1 RECEPTOR

; FILE REFERENCE: GH-70669

; CURRENT APPLICATION NUMBER: US/09/730,931

; CURRENT FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: 60/169,373

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 2

; LENGTH: 427

; TYPE: PRT

; ORGANISM: CANIS FAMILIARIS

US-09-730-931-2

Query Match 94.1%; Score 2087; DB 9; Length 427;

Best Local Similarity 94.1%; Pred. No. 2.2e-191;

Matches 402; Conservative 5; Mismatches 18; Indels 2; Gaps 1;

Qy 1 MEPSATPGAQMGVPPGSRE--PSPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFV 58
 |||
 Db 1 MEPSATPGAQTGTPTGGGELSPSLVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFL 60

Qy 59 VALVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHAL 118
 |||
 Db 61 VALVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHTL 120

Qy 119 CKVIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVP 178
 |||:|
 Db 121 CKVIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARSSILGIWAVSLAVMVP 180
 Qy 179 QAAVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQI 238
 |||:|
 Db 181 QAAVMECSSLPELANRTRLSVCDEHWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQI 240
 Qy 239 FRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAK 298
 |||:|
 Db 241 FRKLWGRQIPGTTSALVRNWKRPDQLEDQGPGLSAEPPPRARAFLAEVKQMRARRKTAK 300
 Qy 299 MLMVLLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIY 358
 |||:|
 Db 301 MLMVLLLVFALCYLPISVLNVLKRVFQSSDREAVYACFTFSHWLVYANSAANPIIY 360
 Qy 359 NFLSGKRFREQKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVLT 418
 |||:|
 Db 361 NFLSGKRFREQKAAFSCCLPGLGPCGSPKAPSPRSSASHKSLSLHRSVSKVPEHVLT 420
 Qy 419 SVTTVLP 425
 |||
 Db 421 SVTTVLP 427

RESULT 11

US-09-828-538-20

; Sequence 20, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.

; APPLICANT: Kwok, Cheni

; APPLICANT: Bodsworth, Nicola J.

; APPLICANT: Halsey, Wendy

; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods

; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications

; FILE REFERENCE: GH-50038-C1

; CURRENT APPLICATION NUMBER: US/09/828,538

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/088,624

; PRIOR FILING DATE: 1998-06-08

; PRIOR APPLICATION NUMBER: 60/093,726

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: 09/328,014

; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 20

; LENGTH: 389

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-828-538-20

Query Match 85.7%; Score 1902.5; DB 9; Length 389;

Best Local Similarity 96.1%; Pred. No. 9.7e-174;

Matches 368; Conservative 2; Mismatches 10; Indels 3; Gaps 2;

Qy 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
 |||
 Db 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
 |||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSLIGIWAIVSLAIMVPQA 180
 |||
 Db 121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSLIGIWAIVSLAIMVPQA 180

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQFKAAFSC-CLPGLGP 382
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 Db 361 LSG--CKEKSALSCPSCPGHDP 381

RESULT 12

US-09-211-823C-23

; Sequence 23, Application US/09211823C

; Publication No. US20030087801A1

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 389

; TYPE: PRT

; ORGANISM: HOMO SAPIENS
US-09-211-823C-23

Query Match 85.7%; Score 1902.5; DB 10; Length 389;
Best Local Similarity 96.1%; Pred. No. 9.7e-174;
Matches 368; Conservative 2; Mismatches 10; Indels 3; Gaps 2;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSAVLTLISFIALDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQA 180
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Db    121 VIPYLQAVSVSAVLTLISFIALDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
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Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAAFSC-CLPGLGP 382
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Db    361 LSG--CKEKSIALSCPSCPGHDP 381
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RESULT 13

US-10-077-874-4

; Sequence 4, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/10/077,874
; FILING DATE: 20-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,509
; FILING DATE: 05-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-077-874-4

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Query Match          85.5%; Score 1897; DB 13; Length 369;
Best Local Similarity 99.7%; Pred. No. 3.1e-173;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
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Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPOA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPOA 180

Qy    181 AVMECSSVLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSVLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KIWGRQIPGTTSLVRNWKRPDQLGDLQGLSGEPQPRARAFLEVKQMRARRKTAKML 300
      |||
Db    241 KIWGRQIPGTTSLVRNWKRPDQLGDLQGLSGEPQPRARAFLEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy     361 LSG 363
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Db     361 LSG 363

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RESULT 14
 US-09-393-696-6

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; Sequence 6, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-393-696-6
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Query Match          85.4%;   Score 1894;   DB 10;   Length 372;
Best Local Similarity 99.4%;   Pred. No. 6e-173;
Matches 361; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGVPPGSRDPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFEGHALCK 120
          ||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFEGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
          ||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          ||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLVPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
          ||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          ||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
          |||
Db    361 LSG 363
```

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RESULT 15
US-10-077-874-6
; Sequence 6, Application US/10077874
; Publication No. US20020115155A1
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; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/077,874
; FILING DATE: 20-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,509
; FILING DATE: 05-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-077-874-6

```

```

Query Match          85.4%; Score 1894; DB 13; Length 372;
Best Local Similarity 99.4%; Pred. No. 6e-173;
Matches 361; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
        |||:|||||
Db      1 MEPSATPGAQMGPVPPGSRDPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRAGSILGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRAGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||

```

Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
 Db 241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSG 363
 |||
 Db 361 LSG 363

Search completed: October 14, 2004, 11:16:34
 Job time : 80.0952 secs

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:41:50 ; Search time 111.535 Seconds
(without alignments)
2192.441 Million cell updates/sec

Title: US-10-070-532-2
Perfect score: 2219
Sequence: 1 MEPSATPGAQMGVPPGSREP.....CSVSKISEHVVLTSVTTVLP 425

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

		8					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	2218	100.0	425	2	Q9HBV6	Q9hbv6 homo sapien	
2	2214	99.8	425	1	OX1R_HUMAN	O43613 homo sapien	
3	2018.5	91.0	416	1	OX1R_RAT	P56718 rattus norv	
4	2015.5	90.8	416	2	Q6VNS3	Q6vns3 mus musculu	
5	2015.5	90.8	416	2	AAR01326	Aar01326 mus muscu	
6	1478.5	66.6	443	2	Q6VLX3	Q6vlx3 mus musculu	
7	1478.5	66.6	443	2	AAR01327	Aar01327 mus muscu	
8	1478.5	66.6	443	2	AAR11294	Aar11294 mus muscu	
9	1478.5	66.6	460	1	OX2R_MOUSE	P58308 mus musculu	
10	1478.5	66.6	460	2	AAR01328	Aar01328 mus muscu	
11	1478.5	66.6	460	2	AAR11293	Aar11293 mus muscu	
12	1474.5	66.4	460	1	OX2R_RAT	P56719 rattus norv	
13	1469	66.2	444	1	OX2R_CANFA	Q9tup7 canis famil	
14	1460	65.8	444	1	OX2R_HUMAN	O43614 homo sapien	
15	1460	65.8	444	2	AAG28021	Aag28021 homo sapi	

16	1287	58.0	364	2	Q8BV78	Q8bv78	mus musculu
17	1261.5	56.8	260	1	OX1R_MOUSE	P58307	mus musculu
18	976	44.0	199	2	Q80T45	Q80t45	mus musculu
19	659.5	29.7	166	2	Q8MJ13	Q8mj13	ovis aries
20	618	27.9	127	2	Q8SPR4	Q8spr4	ovis aries
21	533	24.0	109	2	Q8I010	Q8i010	bos taurus
22	522.5	23.5	430	1	NFF1_HUMAN	Q9gzb6	homo sapien
23	512	23.1	417	1	NFF2_MOUSE	Q924h0	mus musculu
24	508.5	22.9	405	2	Q924N0	Q924n0	mus musculu
25	507.5	22.9	432	1	NFF1_RAT	Q9ep86	rattus norv
26	499.5	22.5	522	1	NFF2_HUMAN	Q9y5x5	homo sapien
27	499	22.5	417	1	NFF2_RAT	Q9eqd2	rattus norv
28	495.5	22.3	399	2	Q75XU5	Q75xu5	gallus gall
29	495.5	22.3	399	2	BAC87782	Bac87782	gallus ga
30	480	21.6	432	2	Q924G9	Q924g9	rattus norv
31	473.5	21.3	758	2	Q7YU49	Q7yu49	drosophila
32	466.5	21.0	427	1	CCKR_RABIT	O97772	oryctolagus
33	452.5	20.4	464	2	Q9VB87	Q9vb87	drosophila
34	452.5	20.4	464	2	AAF56655	Aaf56655	drosophil
35	451	20.3	382	1	NY2R_PIG	O02836	sus scrofa
36	447.5	20.2	449	1	NYR_DROME	P25931	drosophila
37	446	20.1	375	2	O57463	O57463	brachydanio
38	446	20.1	517	2	Q9VWR3	Q9vwr3	drosophila
39	445.5	20.1	353	2	Q7PRC5	Q7prc5	anopheles g
40	444	20.0	542	2	Q9VRM0	Q9vrm0	drosophila
41	444	20.0	542	2	AAF50775	Aaf50775	drosophil
42	443.5	20.0	436	2	Q7T1P8	Q7t1p8	gallus gall
43	438.5	19.8	393	2	Q7T078	Q7t078	fugu rubrip
44	437	19.7	86	1	OX1R_PIG	O97661	sus scrofa
45	436	19.6	370	2	Q6VMN6	Q6vmn6	mus musculu

ALIGNMENTS

RESULT 1

Q9HBV6

ID Q9HBV6 PRELIMINARY; PRT; 425 AA.

AC Q9HBV6;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypocretin receptor-1 (Orexin receptor 1).

GN Name=HCRT1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20429525; PubMed=10973318;

RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,

RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,

RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,

RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;

RT "A mutation in a case of early onset narcolepsy and a generalized

RT absence of hypocretin peptides in human narcoleptic brains.";

RL Nat. Med. 6:991-997(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21580342; PubMed=11723285;
 RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
 RA Stefansson K., Gulcher J.R.;
 RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
 RL Neurology 57:1896-1899(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Olafsdottir B.R., Stefansson R.H., Sigurdsson A., Hannesson H.H.,
 RA Sainz J., Scammell T.E., Stefansson K., Gulcher J.R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yeager M., Welch R., Haque K., Bergen A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF202084; AAG28020.1; -.
 DR EMBL; AF202078; AAG28020.1; JOINED.
 DR EMBL; AF202079; AAG28020.1; JOINED.
 DR EMBL; AF202081; AAG28020.1; JOINED.
 DR EMBL; AF202083; AAG28020.1; JOINED.
 DR EMBL; AF202082; AAG28020.1; JOINED.
 DR EMBL; AF202080; AAG28020.1; JOINED.
 DR EMBL; AY062030; AAL47214.1; -.
 DR EMBL; AY070269; AAL50221.1; -.
 DR EMBL; BC074796; AAH74796.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0016499; F:orexin receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 100.0%; Score 2218; DB 2; Length 425;
 Best Local Similarity 99.8%; Pred. No. 1.4e-144;
 Matches 424; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSRPEPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSRPEPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK	120
Qy	121	VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA	180
Db	121	VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA	180
Qy	181	AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV	420
Db	361	LSGKFREQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV	420
Qy	421	TTVLP	425
Db	421	TTVLP	425

RESULT 2

OX1R_HUMAN

ID OX1R_HUMAN STANDARD; PRT; 425 AA.

AC O43613;

DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).
 GN Name=HCRTR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98150861; PubMed=9491897;
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
 RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
 RA Yanagisawa M.;
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
 RT and G protein-coupled receptors that regulate feeding behavior.";
 RL Cell 92:573-585(1998).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A
 CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be
 CC exclusively coupled to the G(q) subclass of heteromeric G
 CC proteins, which activates the phospholipase C mediated signaling
 CC cascade (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF041243; AAC39601.1; -.
 DR Genew; HGNC:4848; HCRTR1.
 DR MIM; 602392; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0007631; P:feeding behavior; TAS.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.

DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 46 Extracellular (Potential).
 FT TRANSMEM 47 67 1 (Potential).
 FT DOMAIN 68 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 102 2 (Potential).
 FT DOMAIN 103 119 Extracellular (Potential).
 FT TRANSMEM 120 142 3 (Potential).
 FT DOMAIN 143 164 Cytoplasmic (Potential).
 FT TRANSMEM 165 185 4 (Potential).
 FT DOMAIN 186 216 Extracellular (Potential).
 FT TRANSMEM 217 239 5 (Potential).
 FT DOMAIN 240 298 Cytoplasmic (Potential).
 FT TRANSMEM 299 321 6 (Potential).
 FT DOMAIN 322 336 Extracellular (Potential).
 FT TRANSMEM 337 360 7 (Potential).
 FT DOMAIN 361 425 Cytoplasmic (Potential).
 FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 425 AA; 47521 MW; 1634083DE10CA092 CRC64;

Query Match 99.8%; Score 2214; DB 1; Length 425;
 Best Local Similarity 99.5%; Pred. No. 2.6e-144;
 Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSRPEPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGPVPPGSRPEPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFGHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQFKAASFCCPLGPGSLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
          |||
  
```

Db 361 LSGKFREQFKAAFSCLPGLGPCGSLKAPSPRSSASHKSLSLQSRCSISKISEHVVLTSV 420

Qy 421 TTVP 425
 |||||

Db 421 TTVP 425

RESULT 3

OX1R_RAT

ID OX1R_RAT STANDARD; PRT; 416 AA.

AC P56718;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).

GN Name=Hcrtr1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,

RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,

RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,

RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,

RA Yanagisawa M.;

RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides

RT and G protein-coupled receptors that regulate feeding behavior.";

RL Cell 92:573-585(1998).

RN [2]

RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;

RA Hungs M., Mignot E.;

RT "Hypocretin/orexin, sleep and narcolepsy.";

RL Bioessays 23:397-408(2001).

RN [3]

RP REVIEW.

RX MEDLINE=21178476; PubMed=11283317;

RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;

RT "To eat or to sleep? Orexin in the regulation of feeding and

RT wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).

CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A

CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be

CC exclusively coupled to the G(q) subclass of heteromeric G

CC proteins, which activates the phospholipase C mediated signaling

CC cascade.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Highly expressed in the brain in the

CC prefrontal cortex, hippocampus, paraventricular thalamus,

CC ventromedial hypothalamus, arcuate nucleus, dorsal raphe nucleus,

CC and locus coeruleus. Not detected in the spleen, lung, liver,

CC skeletal muscle, kidney and testis. Orexin receptor mRNA

CC expression has also been reported in the adrenal gland, enteric

Qy 181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||||:|||||
 Db 181 AVMECSSVLPELANRTRLFVCDERWADELYPKIYHSCFFVITYLAPLGLMGMAFQIFR 240

Qy 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
 |||||:|||
 Db 241 KLWGPQIPGTTTALVRNWKRPSEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGKFREQKAAAFSCCLPGLGPCGLKAPSPRSSASHKSLSLQSRCSVSKISEHVVLTSV 420
 |||||:|||||
 Db 361 LSGKFREQKAAAFSCCLPGLG-----PSSARHKSLSLQSRCSVSKVSEHVVLTTV 411

Qy 421 TTVL 424
 ||||
 Db 412 TTVL 415

RESULT 4

Q6VNS3

ID Q6VNS3 PRELIMINARY; PRT; 416 AA.
 AC Q6VNS3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeva H.S.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336083; AAR01326.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 416 AA; 46766 MW; A8958C594C365E00 CRC64;

Query Match 90.8%; Score 2015.5; DB 2; Length 416;
 Best Local Similarity 92.0%; Pred. No. 1.2e-130;
 Matches 390; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Query Match 90.8%; Score 2015.5; DB 2; Length 416;
Best Local Similarity 92.0%; Pred. No. 1.2e-130;

Matches 390; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

```
Qy      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
        ||||| ||| | || :|||||:|
Db      1 MEPSATPGAQPGVPTSSGEPFHLPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFLIA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        |||||:|
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
        |||||:|
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAVMVPQA 180

Qy    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||||:|
Db    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
        |||||:|
Db    241 KLWGRQIPGTTSALVRNWKRPSEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVLLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||||:|
Db    301 MVLLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGKFREQKAAFSCLPGLGPCGLKAPSPRSSASHKSLSLQSRCSVSKISEHVLTSTV 420
        |||||:|
Db    361 LSGKFREQKAAFSCLPGLG-----PGSSARHKSLSLQSRCSVSKVSEHVLTSTV 411

Qy    421 TTVL 424
        |||
Db    412 TTVL 415
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RESULT 6

Q6VLX3

```
ID   Q6VLX3      PRELIMINARY;      PRT;      443 AA.
AC   Q6VLX3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Orexin receptor type-2a.
GN   Name=MOXR2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Chen J., Rande H.S.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY339389; AAR11294.1; -.
DR   EMBL; AY339383; AAR11294.1; JOINED.
```

DR EMBL; AY339384; AAR11294.1; JOINED.
 DR EMBL; AY339385; AAR11294.1; JOINED.
 DR EMBL; AY339386; AAR11294.1; JOINED.
 DR EMBL; AY339387; AAR11294.1; JOINED.
 DR EMBL; AY339388; AAR11294.1; JOINED.
 DR EMBL; AY336084; AAR01327.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 66.6%; Score 1478.5; DB 2; Length 443;
 Best Local Similarity 69.7%; Pred. No. 1e-93;
 Matches 287; Conservative 48; Mismatches 68; Indels 9; Gaps 4;

Qy	17	SREPSVPVPDYED-EFLRYLWRDYLYPKQYEWVLI	AAYVAVFVVALVGNTLVCLAVWRNH	75
		:: : :: : : :	: : :	
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLI	AGYIIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES	WLFEGHALCKVIPYLAQAVSVSVAVL	135
			: : : : :	
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITET	WFFGQSLCKVIPYLAQTVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAV	SLAIMVPQAAVMECSSLPELANR	195
		: : : : : :		
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIW	IVSCIIMIPQAIVMECSSLPLGLANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGL	MAMAYFQIFRKLWGRQIPGTTSALV	255
		: :: : : : : : : :		
Db	204	TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLC	LMILAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256	RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVK	QMRARRKTAKMLMVLLVFAICYLP	313
		: : : : : : :		
Db	264	RKWKQQQPVSQ----PRGSGQQSKARISAVAAEIK	QIRARRKTARMLMVLLVFAICYLP	319
Qy	314	ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLV	YANSAANPIIYNFLSGKFREQFKA	373
		: : :		
Db	320	ISILNVLKRVFGMFTHTEDRETVEYAWFTFSHWLV	YANSAANPIIYNFLSGKFREFEKA	379
Qy	374	SCCLPGLGPCGLKAPSPRSSASHKSLSLQ--SRCS	VSKISEHVVLTSVTTV	423
		: : : : : : :		
Db	380	SCCLGVHHRQGDRLARGRTSTESRKSLLTQISN	FDNVSKLSEHVVLTSISTL	431

RESULT 7
 AAR01327

AC AAR11294;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2a.
 GN MOXR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeve H.S.;
 RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2)
 RT gene.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY339383; AAR11294.1; JOINED.
 DR EMBL; AY339384; AAR11294.1; JOINED.
 DR EMBL; AY339385; AAR11294.1; JOINED.
 DR EMBL; AY339386; AAR11294.1; JOINED.
 DR EMBL; AY339387; AAR11294.1; JOINED.
 DR EMBL; AY339388; AAR11294.1; JOINED.
 DR EMBL; AY339389; AAR11294.1; -.
 KW Receptor.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 66.6%; Score 1478.5; DB 2; Length 443;
 Best Local Similarity 69.7%; Pred. No. 1e-93;
 Matches 287; Conservative 48; Mismatches 68; Indels 9; Gaps 4;

Qy	17	SREPSVPVPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH	75
		:: : :: : : : : : :	
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAVL	135
		: : : : : : : : : : : : : : : : : : : : : :	
Db	84	HMRTVTNYFIVNLSLADVLTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPELANR	195
		: : : : : : : : : : : : : : : : : : :	
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSMLPGLANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV	255
		: : : : : : : : :	
Db	204	TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256	RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFAICYLP	313
		: : : : : : : : : : : : : :	
Db	264	RKWKQQQPVSQ----PRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLVFAICYLP	319
Qy	314	ISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAF	373
		:	
Db	320	ISILNVLKRVFQMTHTEDRETVEYAWFTFSHWLVYANSAANPIIYNFLSGKFREFKAAF	379
Qy	374	SCCLPGLGPCGLKAPSPRSSASHKSLSLQ--SRCVSKISEHVVLTSVTTV	423
		: : : : : : : : : : :	

RESULT 9

OX2R_MOUSE

ID OX2R_MOUSE STANDARD; PRT; 460 AA.
AC P58308; Q8BG12;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
GN Name=Hcrtr2; Synonyms=Mox2r;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE OF 100-311 FROM N.A.
RC STRAIN=C57BL/6;
RA Szendro P.I., Maevers K., Eichele G.;
RT "Cloning of mouse orexin receptors.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBDJ databases.
RN [3]
RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [4]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AK038551; BAC30039.1; -.
 DR EMBL; AK048781; BAC33457.1; -.
 DR EMBL; AF394597; AAK71327.1; -.
 DR MGD; MGI:1889024; Mox2r.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 460 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc . .) (Potential).
 FT CONFLICT 201 201 A -> T (in Ref. 2).

FT CONFLICT 240 240 I -> V (in Ref. 2).
SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 66.6%; Score 1478.5; DB 1; Length 460;
Best Local Similarity 69.7%; Pred. No. 1.1e-93;
Matches 287; Conservative 48; Mismatches 68; Indels 9; Gaps 4;

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Qy      17 SREPSVPVPDYED-EFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
          :|| | ||:| |||||:|:|:|:| ||||| | : |||||:| |||:|:|:|
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAVL 135
          |||||:|:|:|:| |||||:|:|:|:| || :|||:| |||||:| |||||:|
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy     136 TLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA AVMC SSVLP ELANR 195
          ||| |||||:|:|:|:| |||:| || || ||:| || |||||:| |||:|
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVVIWIVSCIIMIPQAIVMEC SSM LPLANK 203

Qy     196 TRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALV 255
          | ||:| || | :|||:| |||:|:| || || :| ||||| |||||:| :
Db     204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSV VQ 263

Qy     256 RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFA LCYLP 313
          | || :| | :| : : | | ||:|:| |||||:| |||||:| ||||
Db     264 RKWKQQQPV SQ---PRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLVFAICYLP 319

Qy     314 ISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAF 373
          ||:||||| || || |||||:|:|:|:| |||||:| |||||:| ||||
Db     320 ISILNVLKR VFGMFTHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKAAF 379

Qy     374 SCCLPGLGPCGLKAPSPRSSASHKSLSLQ--SRC SVSKISEHVVLTSVTTV 423
          |||| | | |:| |||:| : :|||:| |||||:|:|:|
Db     380 SCCLGVHHRQGDRLARGRTSTESRKS LTTQISNFDNVSKLSEHVVLTSISTL 431
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RESULT 10

AAR01328

ID AAR01328 PRELIMINARY; PRT; 460 AA.
AC AAR01328;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Orexin receptor type-2b.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chen J., Rande va H.S.;
RT "Cloning and Characterization of the Mouse Type-2b Orexin Receptor
RT Subtype (OX2bR).";
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY336085; AAR01328.1; -.
KW Receptor.

SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 66.6%; Score 1478.5; DB 2; Length 460;
Best Local Similarity 69.7%; Pred. No. 1.1e-93;
Matches 287; Conservative 48; Mismatches 68; Indels 9; Gaps 4;

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QY      17 SREPSVPPDYED-EFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
      ::|| | ||:| |||||:|:|:| ||||| | : |||||:| |||:|:|:|
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

QY      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAVL 135
      |||||:|:|:|:|:|:| ||||:|:|:|:| || :||| |||||:| ||||:|
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

QY     136 TLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQAAMVMECSSLPELANR 195
      ||| |||||:|:|:|:|:| ||: || || ||: || |||||:| |||:
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSLPLGLANK 203

QY     196 TRLESVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
      | ||: |||| | :|||:| |||: ||: || || :|| ||||| |||||:| :
Db     204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ 263

QY     256 RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLP 313
      | || :| | :| : : | | ||:|:| |||||:| |||||:| ||||
Db     264 RKWKQQQPVSQ----PRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLVFALCYLP 319

QY     314 ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKA 373
      ||: ||||| |||| || || ||||| ||||| ||||| ||||| |||||
Db     320 ISILNVLKRVFGMFTHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKA 379

QY     374 SCCLPGLGPCGSLKAPSPRSSASHKSLSLQ--SRCVSKISEHVVLTSVTTV 423
      |||| | | |: | ||: | : :|||: |||||:|:|:|
Db     380 SCCLGVHHRQGDRLARGRTSTESRKS LTTQISNFDNVSKLSEHVVLTSISTL 431
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RESULT 11

AAR11293

ID AAR11293 PRELIMINARY; PRT; 460 AA.
AC AAR11293;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Orexin receptor type-2b.
GN MOXR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chen J., Randeva H.S.;
RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2)
RT gene.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY339383; AAR11293.1; JOINED.
DR EMBL; AY339384; AAR11293.1; JOINED.

RC TISSUE=Brain;
 RX MEDLINE=98150861; PubMed=9491897;
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
 RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
 RA Yanagisawa M.;
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
 RT and G protein-coupled receptors that regulate feeding behavior.";
 RL Cell 92:573-585(1998).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the brain in the cerebral cortex,
 CC septal nuclei, hippocampus, medial thalamic groups, dorsal and
 CC median raphe nuclei, and many hypothalamic nuclei including the
 CC tuberomammillary nucleus, dorsomedial hypothalamus,
 CC paraventricular hypothalamic nucleus, and ventral premammillary
 CC nucleus. Not detected in the spleen, lung, liver, skeletal muscle,
 CC kidney and testis. Orexin receptor mRNA expression has also been
 CC reported in the adrenal gland, enteric nervous system, and
 CC pancreas.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF041246; AAC40042.1; -.
 DR RGD; 2788; Hcrtr2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT	DOMAIN	1	54	Extracellular (Potential).
FT	TRANSMEM	55	75	1 (Potential).
FT	DOMAIN	76	88	Cytoplasmic (Potential).
FT	TRANSMEM	89	110	2 (Potential).
FT	DOMAIN	111	127	Extracellular (Potential).
FT	TRANSMEM	128	150	3 (Potential).
FT	DOMAIN	151	172	Cytoplasmic (Potential).
FT	TRANSMEM	173	193	4 (Potential).
FT	DOMAIN	194	224	Extracellular (Potential).
FT	TRANSMEM	225	247	5 (Potential).
FT	DOMAIN	248	304	Cytoplasmic (Potential).
FT	TRANSMEM	305	327	6 (Potential).
FT	DOMAIN	328	342	Extracellular (Potential).
FT	TRANSMEM	343	366	7 (Potential).
FT	DOMAIN	367	460	Cytoplasmic (Potential).
FT	CARBOHYD	14	14	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	22	22	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	202	202	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	460 AA;	52489 MW;	3B44E3D82F8B85D5 CRC64;

Query Match 66.4%; Score 1474.5; DB 1; Length 460;
 Best Local Similarity 69.8%; Pred. No. 2e-93;
 Matches 286; Conservative 48; Mismatches 71; Indels 5; Gaps 3;

Qy	17	SREPSVPPDYED-EFLRYLWRDYLYPEKQYEWVLI	AAYVAVFVVALVGNTLVCLAVWRNH	75
		:: : : : : :	: : :	
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLI	AGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES	WLFHGHALCKVIPYLQAVSVSVAVL	135
		: : :	:	
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITET	WFFGQSLCKVIPYLTQTVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVS	LAIMVQAAMVMECSSVLPELANR	195
		: : :	: :	
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIV	SCIIMIPQAIVMERSSMLPGLANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLM	AMAYFQIFRKLWGRQIPGTTSALV	255
		: : : :	:	
Db	204	TTLFTVCDERWGGEVYPKMYHICFFLVTYMAPLCLM	VLAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256	RNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMR	RARRKTAKMLMVLLVFALCYLPIS	315
		: : : : : :		
Db	264	RKWKQP--QPVSQPRGSGQQSKARISAVAAEIKQIR	RARRKTARMLMVLLVFALCYLPIS	321
Qy	316	VLNVLKRVFGMFRQASDREAVYACFTFSHWLVYAN	SAANPIIYNFLSGKFREQFAAFSC	375
		: :		
Db	322	ILNVLKRVFGMFTHTEDRETVEYAWFTFSHWLVYAN	SAANPIIYNFLSGKFREFEFAAFSC	381
Qy	376	CLPGLGPCGSLKAPSPRSSASHKSLSLQ--SRCVSK	ISEHVLTSTVTTV	423
		: : : : : :		
Db	382	CLGVHRRQGDRDLARGRTSTESRKSLTTQISNFDNV	SKLSEHVALTSISTL	431

RESULT 13

OX2R_CANFA

ID OX2R_CANFA STANDARD; PRT; 444 AA.

AC Q9TUP7;

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=HCRTR2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99385793; PubMed=10458611;
 RA Lin L., Faraco J., Li R., Kadotani H., Rogers W., Lin X., Qiu X.,
 RA de Jong P.J., Nishino S., Mignot E.;
 RT "The sleep disorder canine narcolepsy is caused by a mutation in the
 RT hypocretin receptor 2 gene.";
 RL Cell 98:365-376(1999).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 RN [4]
 RP VARIANT NARCOLEPSY LYS-54, AND MUTAGENESIS OF GLU-54.
 RX MEDLINE=21180003; PubMed=11282968; DOI=10.1101/gr.161001;
 RA Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;
 RT "Identification and functional analysis of mutations in the hypocretin
 RT (orexin) genes of narcoleptic canines.";
 RL Genome Res. 11:531-539(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Defects in HCRTR2 are a cause of an autosomal recessive
 CC form of narcolepsy, observed in labradors, dobermans and
 CC dachshunds. Narcolepsy is a neurological sleep disorder affecting
 CC animals and humans, characterized by excessive daytime sleepiness,
 CC sleep fragmentation, symptoms of abnormal rapid-eye-movement
 CC (REM) sleep, such as cataplexy, hypnagogic hallucinations, and
 CC sleep paralysis. Cataplexy is a sudden loss of muscle tone
 CC triggered by emotions, which is the most valuable clinical feature
 CC used to diagnose narcolepsy. As in humans, most cases of canine
 CC narcolepsy are sporadic but an autosomal recessive form was also
 CC observed.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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CC -----

DR EMBL; AF164626; AAD49333.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000204; Orexin_receptor.
DR InterPro; IPR004060; Orexin_receptor2.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF03827; Orexin_rec2; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01522; OREXIN2R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Disease mutation; G-protein coupled receptor; Glycoprotein;
KW Transmembrane.
FT DOMAIN 1 54 Extracellular (Potential).
FT TRANSMEM 55 75 1 (Potential).
FT DOMAIN 76 88 Cytoplasmic (Potential).
FT TRANSMEM 89 110 2 (Potential).
FT DOMAIN 111 127 Extracellular (Potential).
FT TRANSMEM 128 150 3 (Potential).
FT DOMAIN 151 172 Cytoplasmic (Potential).
FT TRANSMEM 173 193 4 (Potential).
FT DOMAIN 194 224 Extracellular (Potential).
FT TRANSMEM 225 247 5 (Potential).
FT DOMAIN 248 304 Cytoplasmic (Potential).
FT TRANSMEM 305 327 6 (Potential).
FT DOMAIN 328 342 Extracellular (Potential).
FT TRANSMEM 343 366 7 (Potential).
FT DOMAIN 367 444 Cytoplasmic (Potential).
FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
FT VARIANT 54 54 E -> K (in autosomal recessive
FT narcolepsy).
FT MUTAGEN 54 54 E->K: Loss of function.
SQ SEQUENCE 444 AA; 50675 MW; D848A4536D485D6B CRC64;

Query Match 66.2%; Score 1469; DB 1; Length 444;
Best Local Similarity 69.2%; Pred. No. 4.7e-93;
Matches 286; Conservative 51; Mismatches 66; Indels 10; Gaps 5;

Qy 17 SREPSVPDPDYED-EFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
::|| | ||:| |||||:|:|:| ||||| |: ||||| |||:|:|
Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALVGNVLVCVAVWKNH 83

Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAVL 135
|||||:|:|:| |||:|:|:| ||:| |||:| |||:|
Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy 136 TLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPELANR 195
||| |||||:|:|:| ||: || || |:| ||||:| |||:
Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVIIWIVSCIIMIPQAIVMECSTMLPGLANK 203

Qy 196 TRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
| ||:| ||||| :|||:| |||:|:| || |:| ||||| |||||:| :

Db	204	TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256	RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLVLFALCYLP	313
Db	264	RKWKPLQPASQ----PRGPGQQTKSRI SAVAAEIKQIRARRKTARMLMVLLVFAICYLP	319
Qy	314	ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAFF	373
Db	320	ISILNVLKRVFGMFTHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSGKFFREEFKAFF	379
Qy	374	SCCLPGLGPCGSLKAPSPRSSA-SHKSLSLQ--SRCSVSKISEHVLTSTVTTV	423
Db	380	SCCCLGVHHRQEDRLTRGRSTESRKSLLTQISNFDNVSKLSEQVLTSTL	432

RT wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).

CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF041245; AAC39602.1; -.

DR EMBL; AY062031; AAL47215.1; -.

DR Genew; HGNC:4849; HCRTR2.

DR MIM; 602393; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0008188; F:neuropeptide receptor activity; TAS.

DR GO; GO:0007631; P:feeding behavior; TAS.

DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.

DR GO; GO:0007268; P:synaptic transmission; TAS.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR InterPro; IPR000204; Orexin_receptor.

DR InterPro; IPR004060; Orexin_receptor2.

DR Pfam; PF00001; 7tm_1; 1.

DR Pfam; PF03827; Orexin_rec2; 1.

DR PRINTS; PR00237; GPCRRHODOPSN.

DR PRINTS; PR01522; OREXIN2R.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Glycoprotein; Transmembrane.

FT	DOMAIN	1	54	Extracellular (Potential).
FT	TRANSMEM	55	75	1 (Potential).
FT	DOMAIN	76	88	Cytoplasmic (Potential).
FT	TRANSMEM	89	110	2 (Potential).
FT	DOMAIN	111	127	Extracellular (Potential).
FT	TRANSMEM	128	150	3 (Potential).
FT	DOMAIN	151	172	Cytoplasmic (Potential).
FT	TRANSMEM	173	193	4 (Potential).
FT	DOMAIN	194	224	Extracellular (Potential).
FT	TRANSMEM	225	247	5 (Potential).
FT	DOMAIN	248	304	Cytoplasmic (Potential).
FT	TRANSMEM	305	327	6 (Potential).
FT	DOMAIN	328	342	Extracellular (Potential).
FT	TRANSMEM	343	366	7 (Potential).
FT	DOMAIN	367	444	Cytoplasmic (Potential).
FT	CARBOHYD	14	14	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	22	22	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	202	202	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	444 AA; 50680 MW; CA0669F0D4224C65 CRC64;		

Query Match , 65.8%; Score 1460; DB 1; Length 444;
 Best Local Similarity 68.8%; Pred. No. 1.9e-92;
 Matches 284; Conservative 50; Mismatches 69; Indels 10; Gaps 5;

Qy 17 SREPSVPPDYED-EFLRYLWRDYLKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
 :|| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:|:| |
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCKVIPYQLQAVSVSVAVL 135
 ||||| ||||| |||||:|:|:| || : ||||| ||||:| |
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYQLQTVSVSVSVL 143

Qy 136 TLSFIALDRWYAICHPLLEFKSTARRARGSILGIWAVSLAIMVPQAAMVMECSSLPELANR 195
 ||| |||||:|:|:| ||: || || | :||| ||||:| | ||:
 Db 144 TLSCIALDRWYAICHPLMEFKSTAKRARNISIVIIWIVSCIIMIPQAIVMECSTVFPLANK 203

Qy 196 TRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
 | ||:||||| :|||:| ||:||||| || :|| ||||| ||||:| :
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy 256 RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKMLMVLLLVFALCYLP 313
 | || :| | :| :| | ||:|:| |||||:| |||||:| |||
 Db 264 RKWKPLQPVSQ----PRGPGQPTKSRMSAVAAEIKQIRARRKTARMLMVLLLVFAICYLP 319

Qy 314 ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAP 373
 ||:||||||| ||| ||| ||||| ||||| |||||:| |||
 Db 320 ISILNVLKRVFGMFAHTEDRETVEYAWFTFSHWLVYANSAANPIIYNFLSGKFREFEKAAP 379

Qy 374 SCCLPGLGPCGSLKAPSPRSSA-SHKSLSLQ--SRCSVSKISEHVVLTSVTTV 423
 ||| |: : |:| | ||:| : :||:| ||||:|:|
 Db 380 SCCCLGVHHRQEDRLTRGRTSTESRSLTTQISNFDNISKLSEQVVLTSISTL 432

RESULT 15

AAG28021

ID AAG28021 PRELIMINARY; PRT; 444 AA.
 AC AAG28021;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypocretin receptor-2.
 GN HCRT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20429525; PubMed=10973318;
 RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
 RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
 RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
 RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
 RT "A mutation in a case of early onset narcolepsy and a generalized
 RT absence of hypocretin peptides in human narcoleptic brains."
 RL Nat. Med. 6:991-997(2000).
 DR EMBL; AF202091; AAG28021.1; -.
 DR EMBL; AF202085; AAG28021.1; JOINED.
 DR EMBL; AF202086; AAG28021.1; JOINED.
 DR EMBL; AF202087; AAG28021.1; JOINED.

DR EMBL; AF202088; AAG28021.1; JOINED.
 DR EMBL; AF202089; AAG28021.1; JOINED.
 DR EMBL; AF202090; AAG28021.1; JOINED.
 KW Receptor.
 SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

Query Match 65.8%; Score 1460; DB 2; Length 444;
 Best Local Similarity 68.8%; Pred. No. 1.9e-92;
 Matches 284; Conservative 50; Mismatches 69; Indels 10; Gaps 5;

Qy	17	SREPSVPFPDYED-EFLRYLWRDYLYPEKQYEWVLI	AAYVAVFVVALVGNTLVCLAVWRNH	75
		:: : : : : : : : : :		
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLI	AGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES	WLFQHALCKVIPYLAQAVSVSVAVL	135
		: : : : : : : : :		
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITET	WFFGQSLCKVIPYLAQAVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAV	SLAIMVPAQAAVMECSSLPELANR	195
		: : : : : : :		
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNISIVIIW	IVSCIIMIPQAIAMECSTVFPGLANK	203
Qy	196	TRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLM	AMAYFQIFRKLWGRQIPGTTSALV	255
		: : : : : : : :		
Db	204	TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCL	MVLAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256	RNWK--RPSDQLGDLEQGLSGEPQPRARAFLAEVK	QMRARRKTAKMLMVLLVFALCYLP	313
		: : : : : : :		
Db	264	RKWKPLQPVSQ----PRGPGQPTKSRMSAVAAEIK	QIRARRKTARMLMVLLVFALCYLP	319
Qy	314	ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLV	YANSAANPIIYNFLSGKFREQFKA	373
		: :		
Db	320	ISILNVLKRVFGMFAHTEDRETVEYAWFTFSHWLV	YANSAANPIIYNFLSGKFREFEKA	379
Qy	374	SCCLPGLGPCGSLKAPSPRSSA-SHKSLSLQ--SR	CSVSKISEHVLTSTVTTV	423
		: : : : : : : : :		
Db	380	SCCCLGVHHRQEDRLTRGRTSTESRKSLLTQISN	FDNISKLSEQVLTSTSTL	432

Search completed: October 14, 2004, 10:55:47
 Job time : 113.535 secs